

OM nucleic - nucleic search, using sw model
Copyright (c) 1993 - 2000 Compugen Ltd.
GenCore version 4.5

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

KW Parkinson's disease; eczema; glomerulonephritis; haemorrhage; ischaemia; leukoencephalopathy; infertility; inflammatory eye disease; acute pancreatitis; fibromyalgia; agenesis of corpus callosum.

PD	30-NOV-2000.	XX	640	actttcttcgtttagtcgtcttacccatgtgggttatgcacccatca	69
PF	25-MAY-2000; 2000WO-US14435.	XX	641	actttcttcgtttagtcgtcttacccatgtgggttatgcacccatca	510
PR	25-MAY-1999; 99US-0135158.	XX	700	ggacagccatcttcacceaggagagggctaactaatacaacttactta	759
PR	29-OCT-1999; 99US-0162331.	XX	511	ggacagccatcttcaccaaaaggagggcataactaatacaacttactta	570
PA	(IMMUNEX CORP.	XX	QY	760	gatttctggaaata 774
PI	Sims JE, Renshaw BR;	XX	Db	571	gtttctggaaata 585
DR	WPI; 2001-032039/04.	XX	Ps	p-PSDB; AAB50444.	
PT	Novel interleukin-1 eta polypeptides useful as therapeutic agents for treatment of diseases mediated by polypeptide counter-structure molecules and for identifying inhibitors -	XX	Ps	Claim 1; Page 4; 45pp; English.	
CC	The present sequence encodes an interleukin-1 (IL-1) eta polypeptide.	XX	Ps		
CC	The IL-1 eta polypeptide is useful as a therapeutic agent for the treatment of disease mediated by IL-1 eta polypeptide counter-structure molecules and also for identifying proteins associated with IL-1 eta ligands, to screen for potential inhibitors of activity associated with polypeptide counter-structure molecules and in designing inhibitors.	XX	Ps		
CC	It is used to study cellular processes such as immune regulation, cell proliferation, cell death, cell migration, cell-to-cell interaction and inflammatory responses. IL-1 eta promotes inflammatory responses and is involved in the causation and maintenance of inflammatory and/or autoimmune diseases such as rheumatoid arthritis, inflammatory bowel disease, and psoriasis. IL-1 eta polynucleotides can be used to identify IL-1 eta receptors, to study cell signal transduction and the immune system and to identify genes associated with human conditions such as glaucoma, ectodermal dysplasia, insulin-dependent diabetes mellitus, wrinkly skin syndrome, T-cell leukaemia/lymphoma, and tibial muscular dystrophy.	XX	Ps		
CC	Sequence 585 BP; 161 A; 154 C; 110 G; 160 T; 0 other;	XX	Ps		
SQ		RESULT 3	AAFP83869	ID AAF83869 standard; cDNA; 520 BP.	
		XX	AAFP83869;	AC	
		XX		DT 06-AUG-2001 (first entry)	
		XX		DE Human interleukin-1 receptor antagonist (NOVINTRA B) encoding cDNA.	
		XX		KW NOVX: transmembrane protein; NOVTRN; neuromedin peptide; NOVNUR; gonadotropin-like protein; NOVGN; interleukin-1; NOVINTRA; human; KW cytostatic; neuroprotective; reproductive; antiinflammatory; cancer; KW antibacterial; cerebroprotective; antidiabetic; antiarthritic; antiallermic; antiallergic; ss.	
		XX		OS Homo sapiens.	
		XX		Key Location/Qualifiers	
		XX		FH 3..513	
		XX		FT /*tag= a	
		XX		FT /product= "NOVINTRA B"	
		XX		PN WO200140291-A2.	
		XX		PD 07-JUN-2001.	
		XX		PF 06-DEC-2000; 2000WO-US33029.	
		XX		PR 06-DEC-1999; 99US-0169056.	
		XX		PR 09-DEC-1999; 99US-0169866.	
		XX		PR 09-DEC-1999; 99US-0169886.	
		XX		PR 10-DEC-1999; 99US-0170352.	
		XX		PR 12-JAN-2000; 2000US-0175740.	
		XX		PR 05-DEC-2000; 2000US-0170252.	
		XX		PA (CURA-) CURAGEN CORP.	
		XX		PA Burgess CE, Prayaga SK, Shinkets RA, Rastelli L, Zerhusen BD;	
		XX		PI Mezes PS;	
		XX		DR WPI; 2001-374790/39.	
		XX		DR p-PSDB; AAB5000.	
		XX		Novel isolated human transmembrane, neuromedin peptide gonadotropin-like protein and interleukin-1 receptor antagonist proteins useful for treating cancer, immune response disorder, metabolic function disorders -	
		XX		Claim 8; Fig 12A; 138pp; English.	
		XX			
		CC		The invention provides novel polypeptides (NOVX) selected from human transmembrane protein (NOVNUR), neuromedin peptide (NOVINTRA), gonadotropin-like protein (NOVGN) and two interleukin-1 receptor antagonist proteins (NOVINTRA A and B). The invention also provides methods in which a NOVX polypeptide, polynucleotide and antibody are used in the detection, prevention and treatment of a broad range of pathological states. NOVTRN can be used to treat is a cell signaling disorder such as cancer, immune response disorder, hematopoietic disorder, neurodegenerative disorder. NOVNUR can be used to treat	
		CC			

XX	AC	AAS26842;
XX	DT	07 NOV-2001 (first entry)
DE		Human cDNA encoding a novel
XX		KW Human; immunosuppressive; an
		KW cyrostatic; cardiant; vaso-
		KW neuroprotective; antibacteri-
		KW vulnerable; secreted protein;
		KW hyperproliferative disorder;
		KW cerebrovascular disorder; Alz-
		KW nervous system disorder; Alz-
		KW corrneal infection; wound hea-
		KW skin ageing; food additive;
OS	XX	
PN	XX	
WD	XX	
PD	XX	
PF	17-JAN-2001;	2001WO-US01320.
PR	31-JAN-2000;	2000US0-0179065.
PR	04-FEB-2000;	2000US0-0180628.
PR	24-FEB-2000;	2000US0-0184664.
PR	03-MAR-2000;	2000US0-0184874.
PR	16-MAR-2000;	2000US0-0189674.
PR	17-MAR-2000;	2000US0-0190076.
PR	18-APR-2000;	2000US0-0198123.
PR	19-MAY-2000;	2000US0-0205515.
PR	07-JUN-2000;	2000US0-0209467.
PR	28-JUN-2000;	2000US0-0214886.
PR	30-JUN-2000;	2000US0-0215135.
PR	07-JUL-2000;	2000US0-0216647.
PR	07-JUL-2000;	2000US0-0218880.
PR	11-JUL-2000;	2000US0-0217496.
PR	14-JUL-2000;	2000US0-0218393.
PR	26-JUL-2000;	2000US0-0220963.
PR	14-AUG-2000;	2000US0-022418.
PR	14-AUG-2000;	2000US0-0224213.
PR	14-AUG-2000;	2000US0-0225114.
PR	14-AUG-2000;	2000US0-0225266.
PR	14-AUG-2000;	2000US0-0226267.
PR	14-AUG-2000;	2000US0-0227268.
PR	14-AUG-2000;	2000US0-0225447.
PR	14-AUG-2000;	2000US0-022557.
PR	14-AUG-2000;	2000US0-0227578.
PR	14-AUG-2000;	2000US0-022759.
PR	18-AUG-2000;	2000US0-022529.
PR	22-AUG-2000;	2000US0-0226681.
PR	22-AUG-2000;	2000US0-0228868.
PR	22-AUG-2000;	2000US0-0221182.
PR	23-AUG-2000;	2000US0-0227009.
PR	30-AUG-2000;	2000US0-0224924.
PR	01-SEP-2000;	2000US0-0222887.
PR	01-SEP-2000;	2000US0-0229343.
PR	01-SEP-2000;	2000US0-0223344.
PR	01-SEP-2000;	2000US0-0223144.
PR	05-SEP-2000;	2000US0-0229509.
PR	05-SEP-2000;	2000US0-0222513.
PR	06-SEP-2000;	2000US0-0230437.
PR	08-SEP-2000;	2000US0-0231242.
PR	08-SEP-2000;	2000US0-0231243.
PR	08-SEP-2000;	2000US0-0231244.
PR	08-SEP-2000;	2000US0-0231413.

Search completed: May 13, 2002, 10:55:12
Job time: 40303 sec

Q Sequence 1377 BP; 377 A; 304 C; 316 G; 380 T; 0 other;

Query Match 10.2%; Score 126.4; DB 20; Length 1377;

Matches: 254; **Conservative**: 0; **Mismatches**: 191; **Indels**: 3; **Gaps**: 1

398 *Journal of Health Politics, Policy and Law*, Vol. 30, No. 2, March 2005

351

卷之三

Tue May 14 08:26:35 2002

us-09-723-676-1.rng

Page 14

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: May 13, 2002, 00:03:59 ; Search time 2334.66 Seconds
(without alignments)

11150.494 Million cell updates/sec
Title: US-09-723-676-1
Perfect score: 1244

Sequence: 1 gtgttgccactgtcagtc.....gcatgtcttcaatacctaa 1244
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
listing first 45 summaries
Database : GenEmbl: *
1: gb_ba: *
2: gb_htg: *
3: gb_in: *
4: gb_on: *
5: gb_ov: *
6: gb_patt: *
7: gb_ph: *
8: gb_pi: *
9: gb_pr: *
10: gb_rc: *
11: gb_sts: *
12: gb_sy: *
13: gb_ur: *
14: gb_vr: *
15: em_ba: *
16: em_fnu: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_on: *
21: em_or: *
22: em_ov: *
23: em_patt: *
24: em_ph: *
25: em_pi: *
26: em_rc: *
27: em_sts: *
28: em_un: *
29: em_vr: *
30: em_htg_hum: *
31: em_htg_inv: *
32: em_htg_other: *
33: em_htgo_inv: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match Length	DB ID	Description

RESULT 1
AX167128 AX167128 Sequence 1 from Patent WO0142305. DNA linear PAT 03-JUL-2001
DEFINITION Sequence 1 from Patent WO0142305.
ACCESSION AX167128
VERSION AX167128.1 GI:1456616
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
(bases 1 to 1244)
REFERENCE 1 Welcher, A.A., Luetby, R. and Jing, S.
AUTHORS
TITLE Interleukin-1 receptor antagonist-like molecules and uses thereof
JOURNAL Patent: WO 01/2305-A1 14-JUN-2001;
Amgen Inc. (US)
FEATURES Location/Qualifiers
Source 1. 1244
/organism="Homo sapiens"
/db_xref="dbxref:taxon:9606"
/note="unnamed protein product"

Page 3

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone, and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

The RPCI-11 human B

donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frenzen, E., Tateno, M., Cataneo, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.rgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

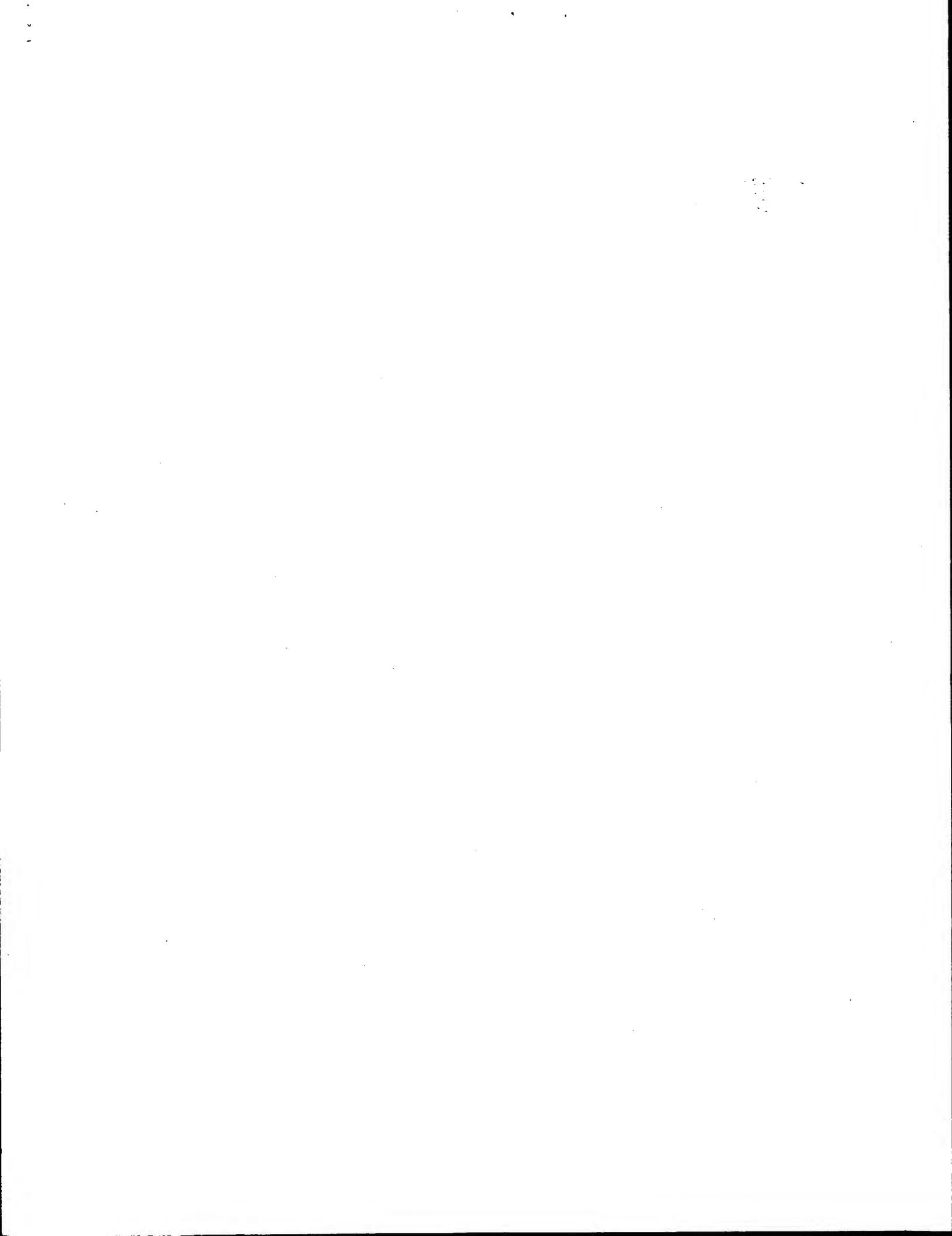
Data from AC084280 and AC024704 was used to finish this clone, AC016724. Polymorphisms have been identified between AC024704 and AC016724.

FEATURES
Source

VERSION	AX193643.1	GI:	15211536
KEYWORDS	.		
SOURCE	pig.		
ORGANISM	<i>Sus scrofa</i>		
REFERENCE	1 (bases 1 to 329)		
AUTHORS	Burgess,C.E., Prayago,S.K., Shimkets,R.A., Rastelli,L., Zerhusen,B.D. and Meier,P.S.		
TITLE	Proteins and nucleic acids encoding the same		
JOURNAL	Patent: WO 0140291-A 65 07-JUN-2001; CurrGen Corporation (US)		
FEATURES	Location/Qualifiers		
source	1..329		
	/organism="Sus scrofa"		
	/db_xref="taxon:9823"		
BASE COUNT	103 a 77 c 64 g 85 t		
ORIGIN			
FEATURES	Location/Qualifiers		
source	1..1190		
	/organism="unidentified"		
BASE COUNT	371 a 227 c 251 g 341 t		
ORIGIN			

PC A61K37/02,A61K37/02,A61K37/02,(C12N15/00,C12R1:91) CC
 Strandedness: Single;
 Topology: Linear;
 FH Key
 FT source 1. .320
 FEATURES s_source /organism="Unidentified"
 BASE COUNT 80 a /db_xref="taxon:32644" 81 c 61 g 91 t 7 others
 ORIGIN
 Query Match 20.2%; Score 251.8; DB 6; Length 320;
 Best Local Similarity 93.8%; Pred. No. 4.1e-60;
 Matches 270; Conservative 0; Mismatches 17; Indels 1; Gaps 1;
 QY 220 taacttctcgctgttagaaaccacggccctcacccacatcgttatctgttttc 279
 Db 23 TCACCTNTCTTCACTTCTAGCCCTCACCACTCATGATCTAATCTNGTCCTNC 82
 QY 280 accaaaggctgtgagacatcatgaccacaacggagragccaaatctatqct 339
 Db 83 ACRAAAGGGCTGTGAAACATCATGAAACCACACGGAGGAGCACCAANRCTATGCT 142
 QY 340 atccgtgattctcgacatgtgtgggtctgtatggaaatttttaatgcgactcc 398
 Db 143 ATTCGTGAAATTCTGCAGATGGTGGCTCTGAGTGAAATTNTTAATGCAGCTC 202
 QY 399 tcttagccggcggatataactgtgtttactgtggaaatttttaatgcgactcc 398
 Db 203 TCTTAGGCCAGCTTAAGCCTGTCACCTCATTTATAGCCIGRAGACACAGATT 262
 QY 459 catgtacaagaaaagggtatatgtgtttactgtggaaatttttaatgcgactcc 506
 Db 263 CAGTGACAGGAAAGGGTATAATGGTTTACCTGGGATCAAGGAA 310
 RESULT 12
 EA1359 AF201831
 LOCUS AF201831
 DEFINITION Homo sapiens FILL epsilon mRNA, complete cds.
 VERSION AF201831
 ACCESSION AF201831.1 GI:6694389
 KEYWORDS SOURCE
 ORGANISM human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 477)
 AUTHORS Smith,D.E., Renshaw,B.R., Ketcham,R.R., Kubin,M., Galka,K.E. and
 Sims,J.E.
 TITLE Four new members expand the interleuin-1 superfamily
 JOURNAL J. Biol. Chem. 275 (2), 1169-1175 (2000)
 MEDLINE 2002888
 REFERENCE 2 (bases 1 to 477)
 AUTHORS Sims,J.E.
 TITLE Direct Submission
 JOURNAL Submitted (04-NOV-1999) Molecular Genetics, Immunex Corporation, 51
 University Street, Seattle, WA 98101, USA
 FEATURES source
 ORIGIN
 Query Match 10.8%; Score 134.2; DB 9; Length 477;
 BASE COUNT 124 a 123 c 117 g 113 t
 ORIGIN
 Best Local Similarity 56.8%; Pred. No. 7.2e-27;

FEATURES s_source
 FT source 1. .320
 FEATURES s_source /organism="Unidentified"
 BASE COUNT 1
 ORIGIN
 Query Match 1
 Best Local Similarity 1
 FT source



OM nucleic - nucleic search, using sw model

Run on: May 12, 2002, 23:46:54 ; Search time 2086.54 Seconds
 (without alignments)
 8046.916 Million cell updates/sec

Score:	1244
Title:	US-09-723-676-1
Sequence:	1 gttgttgcctccactgtcagtc.....gatgttctcttaatccaa 1244
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	13736207 seqs, 678477542 residues
Total number of hits satisfying chosen parameters:	27472414
Minimum DB seq length:	0
Maximum DB seq length:	200000000
Post-processing:	Minimum Match 0%
	Maximum Match 100%
	Listing first 45 summaries

Database :

```

EST:*
1: em_estba:*
2: em_esthun:*
3: em_estin:*
4: em_estiu:*
5: em_espl:*
6: em_estro:*
7: em_htc:*
8: gb_est1:*
9: gb_est2:*
10: gb_htc:*
11: gb_gss:*
12: gb_gss_hum:*
13: em_gss_inv:*
14: em_gss_pln:*
15: em_gss_vrt:*
16: em_gss_vrt:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	531.2	42.7	870	BF244205
2	286.6	23.0	1219	AK009787
3	284.8	22.9	612	BMR86666
4	100.8	8.1	883	AK004061
5	90.6	7.3	475	AZ653999
6	82.2	6.6	536	AW836110
7	82.2	6.6	559	AW578451
8	80.6	6.5	539	AW368430
9	80.6	6.5	555	AW361172
10	80.6	6.5	557	AW368437
11	79.6	6.4	555	BE659560
12	77.4	6.2	436	AW361164
13	73.2	5.9	594	BI951215
14	72	5.8	997	AL557778
15	71.4	5.7	435	W78043
16	70.8	5.7	635	AW262191
17	70.8	5.7	640	BG288796

ALIGMENTS

RESULT	1
LOCUS	BF244205
DEFINITION	601663146F1 NIH_MGC_57 Homo sapiens mRNA clone IMAGE:4080899 5', mRNA sequence.
ACCESSION	BF244205
VERSION	BF244205.1
KEYWORDS	EST.
SOURCE	
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 870)
AUTHORS	NIH MGC http://mgc.ncbi.nih.gov/
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgbps@mail.nih.gov
Tissue	Procurement: ATCC
CDNA Library Preparation:	CLONETECH Laboratories, Inc.
CDNA Library Arrayed by:	The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by:	Incyte Genomics, Inc.
Clone distribution:	MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov .
Plate:	LUCN941 row: k column: 12
High quality sequence stop:	582.
FEATURES	Location/Qualifiers
source	1. -870 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4080899" /clone="NIH_MGC_57" /clone_1ib="NIH_MGC_57" /tissue_type="glioblastoma" /lab_host="l110B (T1 phage-resistant)" /note="Organ: brain; Vector: pDNE-LIB (Clontech); Site_1: SfiI (ggccggctggcc); Site_2: SfiI (ggccatggcc); double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCATTGGCC-3', and 3' adaptor

R-CAL-BUT through R-CAL-BKL, R-CAL-BKB, R-CAL-BKD, R-CAL-BKE,
R-CAL-BLN, R-CAL-BLS, R-CAL-BLF, R-CAL-BLU, R-CAL-BLR through
R-CAL-BLE. The resulting pool represented 20% of the
final driver population. c) a pool of about 15,000 clones
from non-normalized libraries CS0, CTO, CU0, CW0, CX0
and normalized libraries CS0, CTO, CU0, CW0 and CX0
corresponding to plates R-CS0-BD through R-CS0-CBO,
R-CT0-CSAM through R-CT0-CSX, R-CU0-CSB through
R-CU0S-CCA, R-CW0S-CCB through R-CW0S-CCM, R-CX0S-CCN
through R-CX0S-CCX, R-CS0-HSD, R-CS0-BTD through R-CS0-BTV
R-CS0-BVM, R-CT0-BVM through R-CT0-BUP, R-CT0-BVN,
R-CU0-BUO through R-CU0-BVL, R-CW0-BVW through R-CW0-BWP,
R-CV0-BRR, R-CV1-BRS through R-CV1-BSC, R-CV1-BSE through
R-CV1-BTC, and R-CV1-BVO through R-CV1-BXM.
The resulting pool represented 5% of the final driver
population. d) a pool of about 5,000 clones (1,000 from
non-normalized eye library CV0 and 4,000 from normalized
eye library CV1) corresponding to plates R-CV0-BRH through
R-CV0-BRR, R-CV1-BRS through R-CV1-BSC, R-CV1-BSE through
R-CV1-BTC, and R-CV1-BVO through R-CV1-BXM. This pool
represented about 5% of the final driver population. e) A
pool of about 10,000 clones from subtracted library BS2,
BV0 and BV0P (17.9-5 kb cDNA library fraction from rat
whole embryo), and BX0 (0.5-7 kb cDNA library fraction from
rat whole embryo) corresponding to plates R-BS2-BDB
through R-BS2-BFB, R-BVO-ANR through R-BVO-ANR, R-BVO-AOI
through R-BVO-P-AOI, and R-BX0-AOI through R-BX0-AH. The
resulting pool represented 5% of the final driver
population. f) a pool of about 7,000 clones from the
seven non-normalized libraries that make up the tracer
including CY0, C20, DA0, DS0, DC0, DP0, and DE0
corresponding to plates R-CY0-BAP through R-CY0-BXZ,
R-C20-BYA through R-C20-BYT, R-CZ0-BBZ-C, R-DA0-BYJ
through R-DA0-BYP, R-DA0-BZD through R-DA0-BZH, R-DS0-BYQ
through R-DB0-BZA, R-DC0-BZI through R-DC0-BZQ, R-DC0-CAY
through R-DC0-CBA, R-DD0-BZR through R-DD0-CAA,
R-DD0-CBB-C, and R-DE0-CAB through R-DE0-CAL. The
resulting pool represented about 10% of the final driver
population. g) a pool of about 2,000 clones from the pool
of normalized libraries, CN0, that makes up the tracer.
The corresponding plates are R-CNO-BRN through R-CNO-BLD,
R-CNO-BLG, R-CNO-BLP through R-CNO-BLR, R-CNO-BLT,
R-CNO-BLW-X, R-CNO-BMB, and R-CNO-BMF through R-CNO-BML.
This pool represented 5% of the final driver population.
h) a pool of the 28 most abundant clones in the CN0 pool
corresponding to the following addresses: bkwa-a-09-0-UI,
bkw-b-09-0-UI, bkw-b-11-0-UI, bixx-b-10-0-UI, bixx-h-12-0-0-UI
, bixx-d-06-0-UI, bixx-g-08-0-UI, blqg-h-04-0-UI
, bky-a-05-0-UI, bkza-a-06-0-UI, bkza-a-11-0-UI, bizz-c-06-0-UI
, bkz-c-09-0-UI, bkz-d-10-0-0-UI, bla-a-01-0-0-UI,
bla-b-02-0-0-UI, bla-f-04-0-0-UI, bla-g-07-0-0-0-UI, bla-g-12-0-0-UI
, bla-a-12-0-0-UI, bla-f-02-0-0-UI, bla-i-11-0-0-UI, bla-i-11-0-0-UI
, blc-e-95-0-0-UI, blid-a-08-0-0-UI, blid-f-02-0-0-UI, blqg-h-04-0-0-UI
, blt-f-08-0-0-UI, blt-f-08-0-0-UI. This pool represented 5%
of the final driver population. i) One abundant CN0 clone
(corresponding to the address bkz-a-11-0-0-UI) was digested
with Not I and Eco RI and the resulting insert was gel
purified. This purified insert was added directly to the
driver so that it represented 5% of the final driver
population.

TAG_LIB=UI-R-CNL

TAG TISSUE=fundus

TAG SEQ="TCGG"

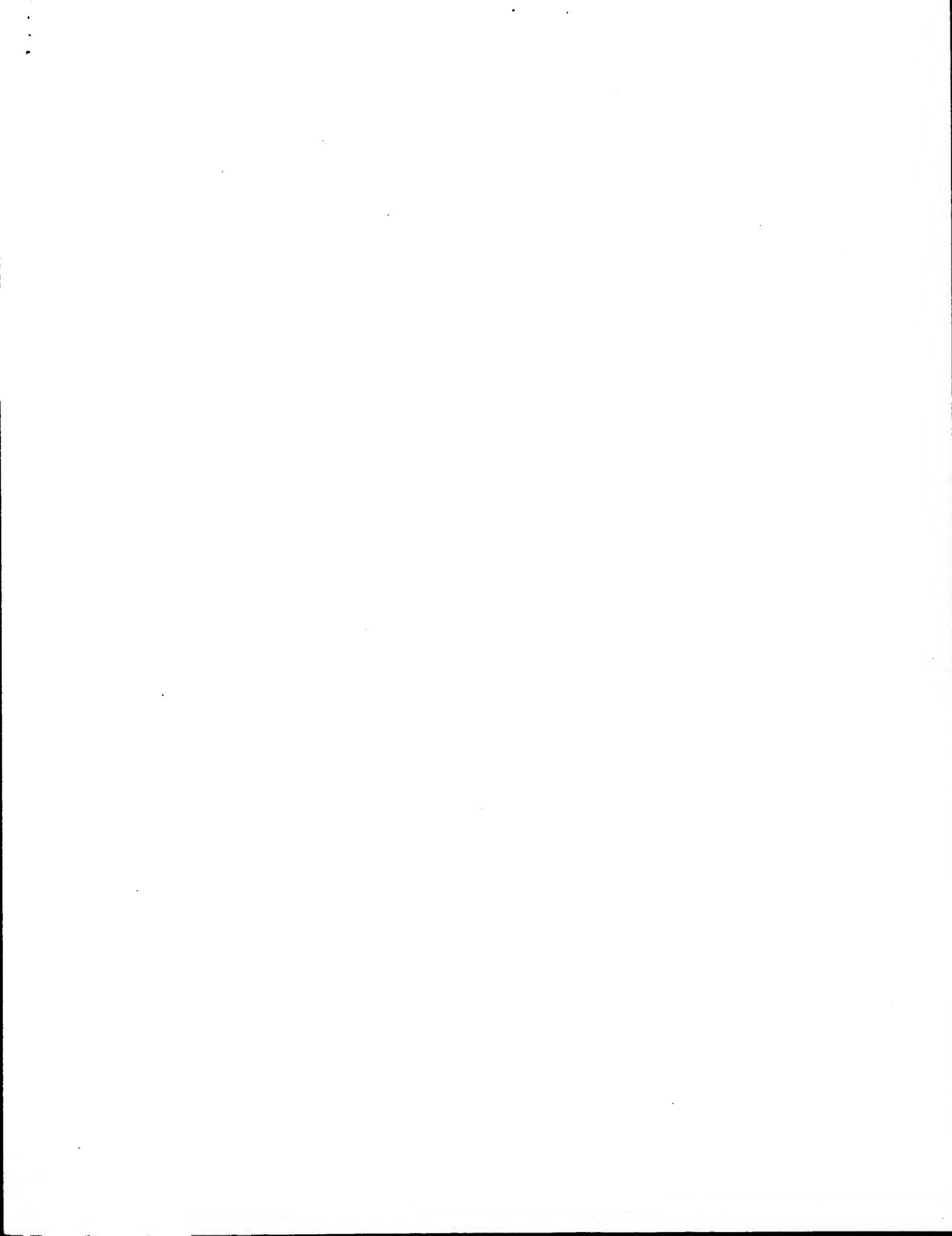
22.9%	Score 284.8;	DB 10;	Length 612;
74.6%	Pred. No. 3..4e-68;		
0;	Mismatches 122;	Indels 0;	Gaps 0;
130 c	124 g	198 t	

QY	420	tgtcaacttcaatatacgctgtaaacacattcgtgaaaggaaaggtaa	479
Db	485	TCTAGTTCTGGGATCAAGGCAGAAGTCCTGCTCGTGTGAGTCGGG	426
QY	540	caagcttacatggaaatcaaggaaaaatcatcgacatgtatggagaagaacg	599
Db	425	CAAACCGACTTGACCTTAAAGGATGAGCATGAACTGAGAACAGC	366
QY	600	acaagaaggcccttctttccacaataaaaggccacttcgttcaatcgagt	659
Db	365	ACAGAAAGCCGTTCTCTACCATGGCATAGGGCATRACTCTGTCCTTCAGCT	306
QY	650	ctcttacacctggctgttcatacgccacccaccatcaggacaggccatcttccac	719
Db	305	CTGTATCTGGCCTTATGCCACCTCTCACAGCAAGAACATCATCTTAC	246
QY	720	caaggaggaggcataactataaacctaactctacttagatgtgtgaataatcca	779
Db	245	ACAGGAGGGTGAAGCTTAACACTACTCTACTCTAGAGCTGAGATACTCA	186
QY	780	gcctaggctgtggggctgtgtccaggatagaatacaagctgtcagtcattaa	839
Db	185	CCATGGCCATATGNGCCAGTGTGAGCCAAAGAACATCAAACCTGTTTAC	126
RESULT	4		
LOCUS	AK004061		
DEFINITION	Mus musculus 18 days embryo mRNA linear HTC 19-JAN-2002		
ACCESSION	AK004061		
VERSION	AK004061.1		
KEYWORDS	GI:12835089		
SOURCE	HTC; CAP trapper.		
ORGANISM	Mus musculus		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
JOURNAL	Carninci,P. and Hayashizaki,Y.		
MEDLINE	High-throughput full-length cDNA cloning		
PUBLMED	Meth. Enzymol. 303, 19-44 (1999)		
REFERENCE	9927953		
AUTHORS	2 (sites)		
TITLE	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.		
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
MEDLINE	Genome Res. 10 (10), 1617-1630 (2000)		
PUBLMED	20499374		
REFERENCE	11042159		
AUTHORS	3 (sites)		
TITLE	Shibata,K., Itoh,M., Aizawa,K., Nagaoaka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kittsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Miyashita,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikeuchi,I., Kashiwagi,K., Fujikawa,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.		
JOURNAL	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer		
MEDLINE	Genome Res. 10 (11), 1757-1771 (2000)		
PUBLMED	2053013		
PUBLMED	11076861		

Query Match	8.1%	Score 100.8;	DB 11;	Length 883;
Best Local Similarity	50.8%	Pred. No. 6e-17	Matches 232;	Indels 0;
Matches 240;	Conservative	0;	Mismatches	0;
LOCUS	303	gaaccacacaaggaggcagcaccaatctatgttatctgttgcacatgtatgt	362	Gaps 0;
DEFINITION	AZ653999	clone UUGCCM0527L124 R, DNA sequence.	362	
ACCESSION	AZ653999		362	
VERSION	AZ653999.1	GT:11791145	362	
KEYWORDS	GSS.		362	
SOURCE	house mouse.		362	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		362	
REFERENCE	1 (bases 1 to 475)		362	
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beaconsfield, T., Duval, B., Hamil, C., Isham, H., Longacre, S., Mahmoud, M., Meenah, E., Pedersen, D., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingay, A., von Niederhäusern, A., and Wright, D., Weiss, R.		362	
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		362	
JOURNAL	Unpublished (2000)		362	
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5605 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0527 row: L column: 24 Seq primer: CACAGGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 475.		362	
FEATURES	Localization/Qualifiers		362	

FEATURES	Source	source
		1. . 997
		/organism="Homo sapiens"
		/db_xref="taxon:9606"
		/clone="SS0D1086YA15"
		/clone_libr="LTL_NF006_PL2"
		/tissue_type="placenta"
		/note="Vector: pcMSPORT 6; site_1: NotI; 1st strand cDNA was printed with a NotI-oligo(dN) primer. Five prime end enriched, double stranded cDNA was digested with Not I and cloned into the Not I and Eco RI sites of the pcMSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com";
BASE COUNT	ORIGIN	BASE COUNT
151 a	172 c	240 a
144 g	127 t	285 c
151 a	144 g	240 g
151 a	144 g	225 t
151 a	144 g	7 others
RESULT	14	RESULT
AL554778	AL554778	15
LOCUS	AL554778	LOCUS
DEFINITION	AL554778 LTL_NFL006_PL2 Homo sapiens mRNA clone CS0D1086YA15 5	DEFINITION
ACCESSION	AL554778	IMAGE:3461775; similar to g9:XE4532_rna INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (HUMAN); mRNA sequence.
VERSION	AL554778.1	VERSION
KEYWORDS	EST.	EST.
ORGANISM	Homo sapiens	ORGANISM
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 435)	REFERENCE
AUTHORS	Hillier,L., Clark,N., Dubique,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kuebba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rikfin,L., Rohlf,M., Soares,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.	AUTHORS
TITLE	The WashU-Merck EST Project	TITLE
JOURNAL	Unpublished (1995)	JOURNAL
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu	COMMENT
FEATURES	Location/Qualifiers	This clone is available royalty-free through LILN ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

FEATURES	Insert Length: 813 Std Error: 0.00 Seq Primer: mob.RIGA+ET Location Qualifiers
Source	1. . 435 /note="Organ: heart; Vector: pRT3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with the Not I - Oligo(dT) primer [TGTGACCAATCTGAGTGGAGCGGCCATCTTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBH19W."
BASE COUNT ORIGIN	97 a 125 c 117 g 95 t 1 others
Query Match	5 7%; Score 71.4; DB 10; Length 435; Best Local Similarity 55.2%; Pred. No. 7 3e-09; Matches 138; Conservative 0; Mismatches 112; Indels 0; Gaps 0;
Oy	473 agggtaatatgttttacccggaaacctaaaggaaaaatctctgtcgagaa 532
Db	38 AGCTCCTGCCTCTGGAAATCCATGGAGGGAGATGTCGCTGTCGTCAGT 97
Oy	513 tcaggaaaccttgcgacttaaggaaaaatcatggaccgtatgtggaga 592
Db	98 CTGTTGAGGAGACGACTCAGCTGGAGGAGTTAACCTACATCTGAGGAGA 157
Oy	593 aaaaaggacacaaaggccctttttccaaataaaggaaacctccatctgttttc 652
Db	158 GAAGCAGGACAAGGCCTCTNCCTCATCCCTCACAGTGCCCCACCCAGTTG 217
Oy	653 agtcagtctttacccctgtggatcatgcacccatccccacacatcaggacacat 712
Db	218 AGCTGCGCCCTGCCCGTTGGTCTCTCCACACGGATGGAAAGCTGACCAGCCGTC 277
Oy	713 ttctcacca 722
Db	278 GCCTCACCAA 287



Copyright (c) 1993 - 2000 Compugen Ltd.

Gencore version 4.5

M nucleic - nucleic search, using sw model

run on: May 12, 2002, 23:38:04 ; Search time 66.4 Seconds (without alignments)

effect score: 1244

sequence: 1 gttgttgcacttcacgtc.....gaatgtttccatcaa 1244

coring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

searched: 383533 seqs, 122816752 residues

total number of hits satisfying chosen parameters: 767066

minimum DB seq length: 0

maximum DB seq length: 200000000

post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_NA:*

- 1: /cggn2_6/ptodata/2/ina/5A_COMB.seq:*
- 2: /cggn2_6/ptodata/2/ina/5B_COMB.seq:*
- 3: /cggn2_6/ptodata/2/ina/5A_COMB.seq:*
- 4: /cggn2_6/ptodata/2/ina/5B_COMB.seq:*
- 5: /cggn2_6/ptodata/2/ina/5CUTS_COMB.seq:*
- 6: /cggn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	324.4	26.1	1190	US-08-939-300-1
2	251.8	20.2	320	US-08-939-300-3
3	125.4	10.2	1183	US-08-790-032-1
4	126.4	10.2	1183	US-09-059-619-1
5	70.8	5.7	462	US-08-790-414-1
6	70.8	5.7	462	US-09-131-247-1
7	70.8	5.7	474	US-08-470-860-9
8	70.8	5.7	474	US-08-910-733-9
9	70.8	5.7	474	US-08-910-884-9
10	70.8	5.7	514	US-08-284-784-41
11	70.8	5.7	514	US-08-854-811-41
12	70.8	5.7	531	US-08-809-185-1
13	70.8	5.7	534	US-09-000-630C-24
14	70.8	5.7	534	US-08-862-730C-24
15	70.8	5.7	543	US-08-422-655-1
16	70.8	5.7	579	US-08-476-860-12
17	70.8	5.7	579	US-08-10-733-12
18	70.8	5.7	579	US-08-910-884-12
19	70.8	5.7	602	US-08-459-811-1
20	70.8	5.7	602	US-08-459-092-1
21	70.8	5.7	602	US-08-459-814-1
22	70.8	5.7	602	US-08-425-232-1
23	70.8	5.7	602	US-08-471-227-2
24	70.8	5.7	603	US-08-844-598-1
25	70.8	5.7	603	US-08-479-140-1
26	70.8	5.7	603	US-08-143-1
27	70.8	5.7	717	US-08-284-784-40

ALIGNMENTS

RESULT	SEQUENCE	PATENT NO.	APPLICANT	INVENTION	NUMBER OF SEQUENCES	CORRESPONDENCE ADDRESS	ADDRESSEE	STREET	CITY	STATE	ZIP	PHONE	COUNTRY	ZIP
1	US-08-939-300-1	1	Application US/08939300	Connor, Janice R.	Family, IL-1 Delta	4	RATNER & PRESTIA	P.O. BOX 980	VALLEY FORGE	PA	19482	610-407-0701	USA	19482

COMPUTER READABLE FORM:

COMPILER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-08/939,300
FILING DATE: 29-SEP-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/046,957
FILING DATE: May 19, 1997

ATTORNEY/AGENT INFORMATION:

NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE DOCKET NUMBER: GH-70018

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 1190 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

Query Match Best Local Similarity 96.8%; Score 324.4; DB 2; Length 1190;

RESULT 11
US-08-854-811-41
; Sequence 41, Application US/08854811
; Patent No. 5914254
; GENERAL INFORMATION:
; APPLICANT: Mascarenhas, Desmond
; APPLICANT: Zhang, Yang
; APPLICANT: Olson, Pamela S.
; APPLICANT: Olsen, David R.
; APPLICANT: Cohen, Pedro A.
; TITLE OF INVENTION: EXPRESSION OF FUSION POLYPEPTIDES
; TITLE OF INVENTION: TRANSPORTED OUT OF THE CYTOPLASM WITHOUT LEADER
; TITLE OF INVENTION: SEQUENCES
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; COMPUTER: IBM Compatible
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,811
; FILING DATE: 12-MAY-1997
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/284,784
; FILING DATE: 02-AUG-1994
; APPLICATION NUMBER: 08/100,744
; FILING DATE: 02-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Buffinger, Nicholas S
; REGISTRATION NUMBER: 39,124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-854-811-41

Query Match 5.7%; Score 70.8; DB 2; Length 514;
Best Local Similarity 52.3%; Pred. No. 2.1e-13;
Matches 181; Conservative 0; Mismatches 162; Indels 3; Gaps 1;

Qy 473 aggtaataatgttttacccgtggaaataaggaaatctctgttcattgtggaaaa 532
Db 158 AGCCCTATGCTGTCCTGGAAATCATGGAGGAGATGCCCTGCTGTCAGT 217
Qy 533 ttcaaggcaagcctactttggagttaaaggaaaatatcatggccatgtggaga 592
Db 218 CTGGTATGAGAACAGACTCCAGCTGGAGGTAAACATCACTGACCTGAGGAACA 277
Qy 593 agaaacacadaaaggccctttttccaaataaagaaggctccacttgttttc 652
Db 278 GAAAGCAGGACAGCCCTGCCTCATCGCCACCCAGTRNG 337
Qy 653 agtcaatgttttacccgtggatcatggaaatccaccacatggacggccat 712
Db 338 AGCTCTGGCCGCGCCGGTGTCTGGAAATCATGGAGGAAGATGRCGTCAGT 397

RESULT 12
US-08-809-185-1
; Sequence 1, Application US/08809185
; Patent No. 5922573
; GENERAL INFORMATION:
; APPLICANT: IL-1 receptor antagonists with increased
; TITLE OF INVENTION: inhibitory activity
; TITLE OF INVENTION: inhibitory activity
; NUMBER OF SEQUENCES: 8
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/M-DOS
; SOFTWARE: Patentin Release #1.0, version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,185
; FILING DATE: 21-SEP-1994
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: IT MI 94/A 001916
; FILING DATE: 21-SEP-1994
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 531 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..531
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1..75
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 76..531
; FEATURE:
; NAME/KEY: mutation
; LOCATION: replace(346..348, "cgc")
; OTHER INFORMATION: /note= "GCC is the codon for the preferred
; OTHER INFORMATION: Ash -> Arg amino acid substitution at this
; OTHER INFORMATION: position."
; FEATURE:
; NAME/KEY: mutation
; LOCATION: replace(400..402, "gcc")
; OTHER INFORMATION: /note= "GCC is the codon for the preferred
; OTHER INFORMATION: Thr -> Ala amino acid substitution at this
; OTHER INFORMATION: position."
; OTHER INFORMATION:
; US-08-809-185-1

Query Match 5.7%; Score 70.8; DB 2; Length 531;
Best Local Similarity 55.2%; Pred. No. 2.2e-13;
Matches 138; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

Qy 473 aggtaataatgttttacccgtggaaataaggaaatctctgttcattgtggaaaa 532
Db 230 AGCTCATGCTGTCCTGGAAATCATGGAGGAAGATGRCGTCAGT 289

RESULT 13

US-09-000-630C-24

; Sequence 24, Application US/09000630C

; Patent No. 6018029

; GENERAL INFORMATION:

; APPLICANT: Fuller, Gerald M

; APPLICANT: Fuentes, Nelson L.

; TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Douglas C Murdock/ Bradley, Arant, Rose & White

; STREET: 2001 Park Place, Suite 1400

; CITY: Birmingham

; STATE: Alabama

; COUNTRY: USA

; ZIP: 35203-2736

; COMPUTER READABLE FORM:

; COMPUTER: IBM compatible

; OPERATING SYSTEM: Microsoft Windows

; SOFTWARE: WordPerfect 6.0

; CURRENT APPLICATION DATA:

; MEDIUM TYPE: Diskette, 3.50 inch,

; COMPUTER: IBM compatible

; OPERATING SYSTEM: Microsoft Windows

; SOFTWARE: WordPerfect 6.0

; CURRENT APPLICATION DATA:

; FILING DATE: 5/23/97

; INFORMATION FOR SEQ ID NO: 24:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 534 base pairs

; STRANDEDNESS: single

; TYPE: nucleic acid

; TOPOLOGY: linear

; MOLECULE TYPE: human IL-1ra DNA sequence

; US-09-000-630C-24.

Query Match 5.7%; Score 70.8; DB 3; Length 534;

Best Local Similarity 55.2%; Pred. No. 2.2e-13; Matches 138; Conservative 0; Mismatches 112; Indels 0; Gaps 0; Gaps 0;

Qy 473 aggtaataggtttacatggaaatacggaaaaatcatggactttgtgcagaaa 532

Db 230 AGCTCTAGCTCTGTTCTGGAAATCCATGGAGATGTCCTGTGCAAGT 289

Qy 533 ttccaggcaagctactttgcacctaaggaaaaataatcatggacctgtatgtgaga 592

Db 290 CTCGGTGAGGACAGCTCAGCTGGAGCAGTAAACACTGAGCTGAGGAACA 349

Qy 593 agaaaggacacaaggccctttttccacataaaggaggccactttgtcttc 652

Db 350 GAAGCGAGCACAGCGCTTGCCTCATCGCAGTGGCCACACCGAGTTG 409

Qy 653 atcaggatcttacccggctgttcacaggccacctccacacatggaggccatct 712

Db 410 AGTCAGCGCCCTGGCCGGTGGTCCCTGACAGCGATGGAAGCTGACAGCGTC 469

Qy 713 ttctcaccaa 722

Db 470 GCCTCACCAA 479

RESULT 14

US-08-862-730C-24

; Sequence 24, Application US/08862730C

; Patent No. 6063600

; GENERAL INFORMATION:

; APPLICANT: Fuller, Gerald M

; APPLICANT: Fuentes, Nelson L.

; TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Douglas C Murdock/ Bradley, Arant, Rose & White

; STREET: 2001 Park Place, Suite 1400

; CITY: Birmingham

; STATE: Alabama

; COUNTRY: USA

; ZIP: 35203-2736

; COMPUTER READABLE FORM:

; COMPUTER: IBM compatible

; OPERATING SYSTEM: Microsoft Windows

; SOFTWARE: WordPerfect 6.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/862,730C

; FILING DATE: 5/23/97

; INFORMATION FOR SEQ ID NO: 24:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 534 base pairs

; STRANDEDNESS: single

; TYPE: nucleic acid

; TOPOLOGY: linear

; MOLECULE TYPE: human IL-1ra DNA sequence

; US-08-862-730C-24.

Query Match 5.7%; Score 70.8; DB 3; Length 534;

Best Local Similarity 55.2%; Pred. No. 2.2e-13; Matches 138; Conservative 0; Mismatches 112; Indels 0; Gaps 0; Gaps 0;

Qy 473 aggtaataggtttacatggaaatacggaaaaatcatggactttgtgcagaaa 532

Db 230 AGCTCTAGCTCTGTTCTGGAAATCCATGGAGATGTCCTGTGCAAGT 289

Qy 533 ttccaggcaagctactttgcacctaaggaaaaataatcatggacctgtatgtgaga 592

Db 290 CTCGGTGAGGACAGCTCAGCTGGAGCAGTAAACACTGAGCTGAGGAACA 349

Qy 593 agaaaggacacaaggccctttttccacataaaggaggccactttgtcttc 652

Db 350 GAAGCGAGCACAGCGCTTGCCTCATCGCAGTGGCCACACCGAGTTG 409

Qy 653 atcaggatcttacccggctgttcacaggccacctccacacatggaggccatct 712

Db 410 AGTCAGCGCCCTGGCCGGTGGTCCCTGACAGCGATGGAAGCTGACAGCGTC 469

Qy 713 ttctcaccaa 722

Db 470 GCCTCACCAA 479

RESULT 15

US-08-422-655-1

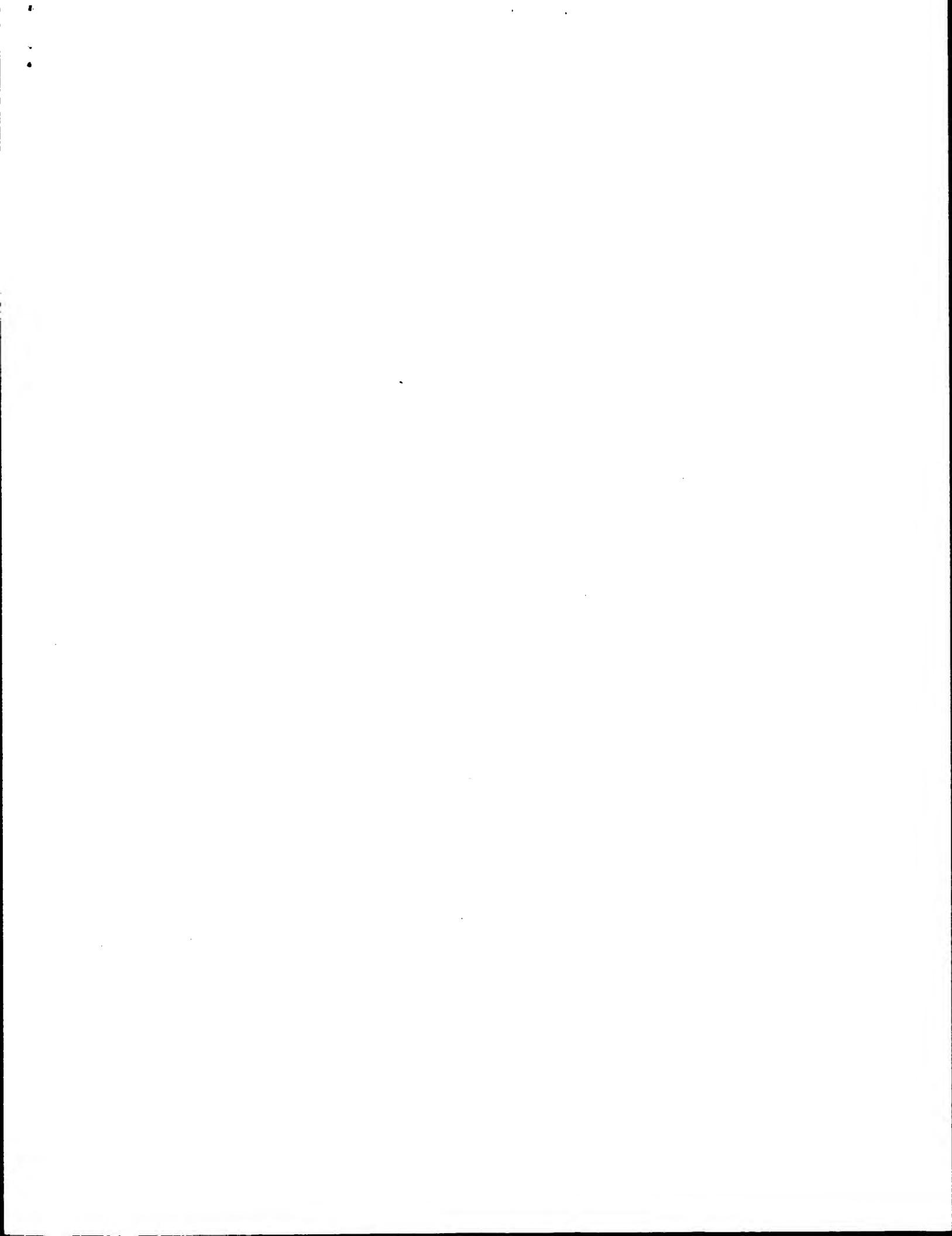
; Sequence 1, Application US/08422655

; Patent No. 5747072

; GENERAL INFORMATION:

; APPLICANT: Davidson, Beverly L.

Search completed: May 13, 2002, 10:50:58
Job time: 40374 sec



OM protein - protein search, using sw model
 Run on: May 10, 2002, 09:09:50 ; Search time 23.76 Seconds
 (without alignments)
 Scoring table: BLOSUM62 FLLTKERGINNTNFYLDSSVE 157
 Searched: 52463 seqs, 74073290 residues
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

SUMMARIES

ALIGNMENTS

RESULT	1
AAE04299	standard; Protein; 157 AA.
ID	
XX	
AC	AAE04299;
XX	
DT	04-SEP-2001 (first entry)
DE	Human Interleukin-1 Receptor Antagonist-Like (IL-1ra-L).
XX	
KW	Human; Interleukin-1 Receptor Antagonist-Like; IL-1ra-L; atherosclerosis; multiple sclerosis; septic shock; anorexia; psoriasis; osteoporosis; emphysema; Alzheimer's disease; gene therapy; tranquilliser; pulmonary; cytostatic; rheumatoid arthritis; autoimmune disease; diabetes; leprosy; pulmonary tuberculosis; septicemia; cachexia; hypoglycemia; lung injury; Parkinson's disease; eczema; glomerulonephritis; haemorrhage; ischaemia; leukaemia; infertility; inflammatory eye disease; acute pancreatitis; fibromyalgia.
XX	
OS	Homo sapiens.
XX	
PN	WO200142305-A1.
XX	
PD	14-JUN-2001.
XX	
PF	28-NOV-2000; 2000WO-US32400.
XX	
PR	10-DEC-1999; 99US-0170052.
XX	
PR	28-NOV-2000; 2000US-0170052.
XX	
PA	(AMGE-) AMGEN INC.
XX	
PI	Welcher AA, Lutthy R, Jing S;
XX	

DR WPI: 2001-417857/44.
 DR N-PSDB; AAC08531.
 XX
 PT Novel interleukin-1 receptor antagonist-like polypeptide, its fragment,
 variant useful for treating multiple sclerosis, septic shock, anorexia,
 PT Alzheimer's disease, emphysema, psoriasis, osteoporosis,
 PT atherosclerosis -
 XX
 PS Claim 14; Fig 1; 133pp; English.
 XX
 CC The present sequence is human Interleukin-1 receptor antagonist-like (IL-
 CC Ira-L) protein encoded by IL-1ra-L cDNA (ATCC Deposit No: PTA-1215). IL-
 CC Ira-L DNA and protein are useful for treating, diagnosing, preventing or
 ameliorating disorders or conditions involving immune system dysfunction
 CC (rheumatoid arthritis, inflammatory arthritis, autoimmune disease,
 CC multiple sclerosis, diabetes, transplant rejection), infections (leprosy,
 liver, septicemia or septic shock); weight disorders (obesity, anorexia,
 CC cachexia, hypoglycaemia); neuronal dysfunctions (Alzheimer's disease,
 CC Parkinson's disease); lung (acute or chronic lung injury); skin (eczema,
 CC psoriasis); kidney (acute and chronic glomerulonephritis); bone
 CC (osteoporosis, osteopetrosis); vascular system (haemorrhage, ischaemia,
 CC hemorrhagic shock, atherosclerosis, congestive heart failure); tumour
 CC cells (leukaemia); reproductive system (infertility); eye (inflammatory
 CC eye disease). IL-1ra-L DNA and protein are also useful for treating
 CC acute pancreatitis, acute fatigue syndrome or fibromyalgia. IL-1ra-L DNA
 CC is useful in gene therapy techniques and chromosome mapping.
 XX Sequence 157 AA;

Query Match 100.0%; Score 818; DB 22; Length 157;
 Best Local Similarity 100.0%; Pred. No. 5.8e-83;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPOREAAPKSYAIRDSRQWVWLGSNSLIAAPLSRSIKPVTLHLLACRDTESDKEKG
 Db 1 mnpgreadapksyairdsrqnwvwlgsnslaaplsrsikpvthllacrdtetsdkekgn 60
 QY 61 MWYLIGIKGDLCFLCAETOGKPTIQLKEKNIMDLVEKKQKPELFHNREGSTSVFQSV 120
 Db 61 myylgikgkdlclfcaeiqgkptiqlkeknnimdyvekkqkpfifffhnregstsvfqsv 120
 QY 121 SYPGWFATSTSGQPILTKERGITNNNTFYLDSE 157
 Db 121 sypgwfiatstsgqpifiltergtnntnyldse 157

RESULT 2

AAB5044 AAB5044 standard; Protein; 157 AA.

XX
 AC AAB5044;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE Human IL-1 eta.
 XX
 KW Human; IL-1; interleukin-1; IL-1 eta; immunosuppressive;
 KW antiinflammatory; antiarthritic; antipsoriatic; inflammation;
 KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
 KW psoriasis.

XX Homo sapiens.

XX WO200071720-A1.

PD 30-NOV-2000.

XX 25-MAY-2000; 2000WO-US14435.

XX 25-MAY-1999; 99US-0135758.

PR 29-OCT-1999; 99US-0162331.

XX PA (IMAV) IMMUNEX CORP.
 XX PI Sims JE, Renshaw BR;
 XX WPI: 2001-032339/04.
 DR N-PSDB; AAC90487.

PT Novel interleukin-1 eta polypeptides useful as therapeutic agents for
 treatment of diseases mediated by polypeptide counter-structure
 molecules and for identifying inhibitors -
 XX
 PS Claim 4; Page 5; 45pp; English.
 XX
 CC The present sequence is an interleukin-1 (IL-1) eta polypeptide.
 CC The IL-1 eta polypeptide is useful as a therapeutic agent for the
 treatment of disease mediated by IL-1 eta polypeptide counter-structure
 molecules and also for identifying proteins associated with IL-1 eta
 CC ligands, to screen for potential inhibitors of activity associated with
 polypeptide counter-structure molecules and in designing inhibitors.
 CC It is used to study cellular processes such as immunoregulation, cell
 proliferation, cell death, cell migration, cell-to-cell interaction and
 CC inflammatory responses. IL-1 eta promotes inflammatory responses and is
 involved in the causation and maintenance of inflammatory and/or
 CC autoimmune diseases such as rheumatoid arthritis, inflammatory bowel
 disease, and psoriasis. IL-1 eta polynucleotides can be used to identify
 CC IL-1 eta receptors, to study cell signal transduction and the
 CC immune system and to identify genes associated with human conditions
 CC such as glaucoma, ectodermal dysplasia, insulin-dependent diabetes
 CC muscular dystrophy.
 XX Sequence 157 AA;

Query Match 100.0%; Score 818; DB 22; Length 157;
 Best Local Similarity 100.0%; Pred. No. 5.8e-83;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPOREAAPKSYAIRDSRQWVWLGSNSLIAAPLSRSIKPVTLHLLACRDTESDKEKG
 Db 1 mnpgreadapksyairdsrqnwvwlgsnslaaplsrsikpvthllacrdtetsdkekgn 60
 QY 61 MWYLIGIKGDLCFLCAETOGKPTIQLKEKNIMDLVEKKQKPELFHNREGSTSVFQSV 120
 Db 61 myylgikgkdlclfcaeiqgkptiqlkeknnimdyvekkqkpfifffhnregstsvfqsv 120
 QY 121 SYPGWFATSTSGQPILTKERGITNNNTFYLDSE 157
 Db 121 sypgwfiatstsgqpifiltergtnntnyldse 157

RESULT 3

AAB85000 AAB85000 standard; Protein; 170 AA.

XX AC AAB85000;
 XX DT 06-AUG-2001 (first entry)

DE Human interleukin-1 receptor antagonist (NOVINTRA B) polypeptide.

KW NOVX; transmembrane protein; NOVRAN; neuropeptide; NOVNEUR;
 KW gonadotropin-like protein; NOVGN; interleukin-1; NOVINTRA; human;
 KW cytosolic; neuroprotective; anti-inflammatory; cancer;
 KW antibacterial; cerebroprotective; antidiabetic; antiarthritic;
 KW antiasthmatic; antiallergic.
 XX Homo sapiens.

XX WO200140291-A2.

PD 07-JUN-2001.

XX	06-DIC-2000;	2000WO-US33029.			
PR	05-DIC-1999;	99US-0169056.			
PR	09-DIC-1999;	99US-0169866.			
PR	09-DIC-1999;	99US-0169886.			
PR	10-DIC-1999;	99US-0170252.			
PR	12-JAN-2000;	2000US-0175740.			
PR	05-DIC-2000;	2000US-0170252.			
XX					
XX	(CURA-)	CURAGEN CORP.			
XX	Burgess CE,	Prayaga SK,	Shimkets RA,	Rastelli L,	Zerhusen BD;
PI	Mezes PS;				
XX					
WPI;	2001-374790/39.				
DR	N-PSDB; AAF83869.				
XX					
PT	Novel isolated human transmembrane, neuromedin peptide gonadotropin-like protein and interleukin-1 receptor antagonist proteins, useful for treating cancer, immune response disorder, metabolic function disorders -				
PT	Claim 1; Fig 12B; 138pp; English.				
XX					
CC	The invention provides novel polypeptides (NOVX) selected from human transmembrane protein (NOVTRAN), neuromedin peptide (NOVNEUR), gonadotropin-like protein (NOVGOMY) and two interleukin-1 receptor antagonist proteins (NOVINTRA A and B). The invention also provides methods in which a NOVX polypeptide, polynucleotide and antibody are used in the detection, prevention and treatment of a broad range of pathological states. NOVTRAN can be used to treat 1s a cell signaling disorder such as cancer, immune response disorder, hematopoietic disorder, neurodegenerative disorder. NOVNEUR can be used to treat endocrine disorder, muscle disorder, neurologic disorder, cancers of central nervous system, breast, colon, ovary, kidney, prostate and thyroid. NOVGOM can be used to treat reproductive development disorder, metabolic function disorder or structure disorder, inflammatory response disorder, immune regulation disorder, septic shock, stroke, diabetes, arthritis and cancer. The present sequence represents the NOVINTRA B polypeptide.				
XX					
SQ	Sequence 170 AA:				
Query Match	95.0%;	Score 777;	DB 22;	Length 170;	
Best Local Similarity	100.0%;	Pred. No. 2.3e-78;			
Matches	149;	Conservative 0;	Mismatches 0;	Indels 0;	
Gaps	0;				
XX					
Qy	9 PRSYAIRSRQMWLQLSGNLSIAPLSRSIKPVTLHILACRTEFSDEKEKGNNVYLGIKG 68				
Db	22 pksyairdsrqmvwvlsgnlsiaplrsikpvthilaciadtefsdkekgnvylgkg 81				
XX					
Qy	69 KOLCLFCREIQGKPLQIQLKEKNMDLYKEVKAQKPLFLFINKEGSTSVFQSYSYRGWFA 128				
Db	82 kdclfciaeigqkplqlqekknmdlyvekkaqkpfllfinkegstsvfqsysypwfia 141				
XX					
Qy	129 TSTTSGOPFLTERGIGNTNTNFYIDSVE 157				
Db	142 tstsgrqpliftergigntntnfldsve 170				
XX					
RESULT	4				
ID	AAW82542				
ID	AAW82542 standard; Protein; 164 AA.				
XX					
AC	AAW82542;				
DT	08-FEB-1999 (first entry)				
XX					
DE	Human IL-1 delta protein.				
XX					
RESULT	5				
ID	AYY70217				
ID	AYY70217 standard; Protein; 158 AA.				
XX					
AC	AYY70217;				
XX					
DT	06-JUN-2000 (first entry)				
XX					
XX	Interleukin-1; IL-1 delta; human; diagnosis; immunise; vaccine; stroke; inoculate; inflammation; arthritis; septicemia; autoimmune disease; inflammatory bowel disease; psoriasis; transplant rejection; infection; graft versus host disease; ischema; acute respiratory disease syndrome; restenos; brain injury; AIDS; bone disease; osteoporosis; cancer; lymphoproliferative disorder; arteriosclerosis; Alzheimer's disease; mapping; linkage.				
XX					
OS	Homo sapiens.				
XX					
EP	EP879889-A2.				
PN					
XX					
PD	25-NOV-1998.				
XX					
PF	17-FEB-1998;	98EP-0301169.			
XX					
PR	29-SEP-1997;	97US-0939300.			
PR	19-MAY-1997;	97US-0046957.			
XX					
PA	(SMIK) SMITHKLINE BEECHAM CORP.				
XX					
PT	Connor JR, James IE, Young PR;				
XX					
DR	WPI; 1998-596881/51.				
DR	N-PSDB; AAV69326.				
XX					
PT	New IL-1 delta polypeptide and polynucleotide - useful as diagnostic reagents and for diagnosing, prevention or treatment of cancer, AIDS or Alzheimer's disease				
PT	Claim 1; Page 18; 21pp; English.				
XX					
CC	This sequence represents a novel human interleukin-1 polypeptide, IL-1 delta, (interleukin-1 delta). IL-1 delta polypeptides and polynucleotides are useful for diagnosing susceptibility to diseases by detecting mutations in the IL-1 delta gene. IL-1 delta antibodies are useful for inducing an immune response to immunize and prevent diseases, and for isolating IL-1 delta clones or purifying the polypeptides by affinity chromatography. IL-1 delta polypeptides can be administered directly or as a vaccine to inoculate against disease. Diseases diagnosed, prevented or treated include: chronic and acute inflammation, arthritis, septicemia, autoimmune diseases e.g. inflammatory bowel disease, psoriasis, transplant rejection, graft versus host disease, infection, stroke, ischemia, acute respiratory disease syndrome, restenos, brain injury, AIDS, bone diseases e.g. osteoporosis, cancer e.g. lymphoproliferative disorders, atherosclerosis and Alzheimer's disease. The IL-1 delta polypeptide is also useful for mapping the gene to a chromosome, allowing gene inheritance to be studied through linkage analysis.				
CC					
CC	Sequence 164 AA:				
XX					
Query Match	55.3%;	Score 452;	DB 19;	Length 164;	
Best Local Similarity	94.6%;	Pred. No. 2.7e-42;			
Matches	88;	Conservative 1;	Mismatches 4;	Indels 0;	
Gaps	0;				
XX					
Qy	1 MNPOREAKPSAIRDQMWLQLSGNSLTAAULRSIKPVTLHILACRTEFSDEKEGN 60				
Db	1 mnpoqreakpsyairdsrqmvwvlsgnlsiaplrsikpvthilaciadtefsdkekgn 60				
XX					
Qy	61 MVLGLRGKDCIFCAETQGKPLQLKRNIM 93				
Db	61 mvylgikgkdclclfciaeigqkplqlkqgsq 93				
XX					

XX
DE Human Interleukin-1 epsilon protein.
XX
KW Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;
KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;
KW gene mapping; immune system; treatment; inflammatory disease;
KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
KW psoriasis; human.
XX
OS Homo sapiens.
XX
PN WO200011174-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US18771.
XX
PR 21-AUG-1998; 98US-0097413.
PR 31-AUG-1998; 98US-0098595.
PR 11-SEP-1998; 98US-0099574.
PA (IMMV) IMMUNEX CORP.
XX
PI Sims JE, Smith DE;
XX
DR WPI; 2000-237653/20.
DR N-PSDB; AAZ51247.
XX
PT Nucleotide sequences encoding human interleukin -1 epsilon, useful to
PT treat inflammatory and immune system-related diseases such as
PT rheumatoid arthritis and inflammatory bowel disease -
PS Claim 1b; Fig 2; 76pp; English.
XX
CC The present sequence is that of human Interleukin-1 (IL-1) epsilon
CC expressed in spleen, lymph node, thymus, tonsil and leucocyte
CC tissues. IL-1 epsilon is a cytokine, with antiinflammatory,
CC immunosuppressant, antirheumatic, antiarthritic and antipsoriatic
CC activity. It can be used in the treatment of inflammatory or autoimmune
CC diseases such as rheumatoid arthritis, inflammatory bowel disease and
CC psoriasis. The DNA sequence can be used in chromosome identification,
CC gene mapping and study of immune system.
XX
Sequence 158 AA;

Query Match
Best Local Similarity 47.1%; Score 385; DB 21; Length 158;
Matches 71; Conservative 29; Mismatches 45; Indels 0; Gaps 0;

Qy 9 PKSYAIRDPSROMWVWLGSNLIAAPLRSIKPVTLHLIACRTEFSDKEKGNNMYLGIGK 68
Db 10 pgqsgsqdinhrrvwlqdqtliavprkrdrmsptvtialiscrvhetekdrqnpiyqlng 69
Qy 69 KDLCLFCARIQKPTLQLKEKNMDLVKEKAQKPLFFHNEKGSTSVFQSVPGWFTA 128
Db 70 lnlcimcakvqdqptlqekdmldlnqpepkvsflfynsqsgnrfesvafpgwfia 129
Qy 129 TSTTSQPIFLTNERGTTNTNFYL 153
Db 130 vsseggcpliltqelgkanttdfgl 154

RESULT 6
ID AAY70218 standard; Protein; 158 AA.
XX
AC AAY70218;
DT 06-JUN-2000 (first entry)
XX
DE Human Interleukin-1 epsilon polymorphic variant.

XX
DE Human Interleukin-1 epsilon protein.
XX
KW Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;
KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;
KW gene mapping; immune system; treatment; inflammatory disease;
KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
KW psoriasis; polymorphic variant; human.
XX
OS Homo sapiens.
XX
FH FT Key
FT FT Misc-difference 12 Location/Qualifiers
XX FT FT /note= "Wild type Glu replaced with Arg"
XX PN WO200011174-A1.
XX PD 02-MAR-2000.
XX PR 20-AUG-1999; 99WO-US18771.
XX PR 21-AUG-1998; 98US-0097413.
PR 31-AUG-1998; 98US-0098595.
PR 11-SEP-1998; 98US-0099574.
PA (IMMV) IMMUNEX CORP.
XX
PI Sims JE, Smith DE;
XX
DR WPI; 2000-237653/20.
DR N-PSDB; AAZ51248.
XX
PT Nucleotide sequences encoding human interleukin -1 epsilon, useful to
PT treat inflammatory and immune system-related diseases such as
PT rheumatoid arthritis and inflammatory bowel disease -
PS Claim 1b; Fig 2; 76pp; English.
XX
CC The present protein sequence is that of human Interleukin-1 (IL-1)
CC epsilon polymorphic variant. IL-1 epsilon gene is mapped to chromosome 2q
CC and is mainly expressed in spleen, lymph node, thymus, tonsil and
CC leucocyte tissues. IL-1 epsilon is a cytokine, with antiinflammatory,
CC immunosuppressant, antirheumatic, antiarthritic and antipsoriatic
CC activity. It can be used in the treatment of inflammatory or autoimmune
CC diseases such as rheumatoid arthritis, inflammatory bowel disease and
CC psoriasis. The DNA sequence can be used in chromosome identification,
CC gene mapping and study of immune system.
XX
Sequence 158 AA;

Query Match
Best Local Similarity 46.9%; Score 384; DB 21; Length 158;
Matches 71; Conservative 29; Mismatches 45; Indels 0; Gaps 0;

Qy 9 PKSYAIRDPSROMWVWLGSNLIAAPLRSIKPVTLHLIACRTEFSDKEKGNNMYLGIGK 68
Db 10 pgqsgsqdinhrrvwlqdqtliavprkrdrmsptvtialiscrvhetekdrqnpiyqlng 69
Qy 69 KDLCLFCARIQKPTLQLKEKNMDLVKEKAQKPLFFHNEKGSTSVFQSVPGWFTA 128
Db 70 lnlcimcakvqdqptlqekdmldlnqpepkvsflfynsqsgnrfesvafpgwfia 129
Qy 129 TSTTSQPIFLTNERGTTNTNFYL 153
Db 130 vsseggcpliltqelgkanttdfgl 154

RESULT 7
ID AAE03417
ID AAE03417 standard; Protein; 273 AA.
XX
AC AAE03417;
XX
DT 03-AUG-2001 (first entry)

XX DE Human interleukin-1 receptor antagonist-like (IL-1ra-L).
 XX
 KW Human; interleukin-1 receptor antagonist-like protein; IL-1ra-L; therapy;
 KW rheumatoid arthritis; psoriatic arthritis; inflammatory arthritis; lupus;
 KW joint disease; autoimmune disease; multiple sclerosis; diabetes; obesity;
 KW transplant rejection; graft versus host disease; strain; sprain; leprosy;
 KW cartilage damage; hepatitis; human immunodeficiency virus; HIV; anorexia;
 KW clostridium-associated diarrhoea; pulmonary tuberculosis; septic shock;
 KW myopathy; Alzheimer's disease; Parkinson's disease; memory disorder;
 KW acute respiratory disease syndrome; cystic fibrosis; asthma; psoriasis;
 KW eczema; glomerulonephritis; osteoporosis; Paget's disease; lymphoma;
 KW hypercalcaemia; haemorrhage; ischaemia; atherosclerosis; leukaemia;
 KW infertility; endometriosis; retinal neuropathy; acute pancreatitis;
 KW Kawasaki's disease; cancer.
 XX OS Homo sapiens.
 PN WO200141732-A1.
 XX PR 10-DEC-1999; 99US-0170105.
 XX PR 28-NOV-2000; 2000US-0724859.
 XX PA (AMGE-) AMGEN INC.
 XX PI Calzone FJ, Luethy R, Boedigheimer MJ, zhu J, Chung Y, Jing S;
 XX PT WPI; 2001-381495/40.
 DR N-PSDB; AAB06911.
 XX PT Novel Interleukin-1 Receptor Antagonist-Like nucleic acid molecule, the
 PT polypeptide encoded by the nucleic acid is useful diagnosis, treatment,
 PT and prevention of diseases such as arthritis, diabetes, transplant
 PT rejection.
 XX PS Claim 13; FIG 1A; 127pp; English.
 XX CC The present sequence is human interleukin-1 receptor antagonist-like
 CC (IL-1ra-L) protein. IL-1ra-L is useful for treating, preventing or
 CC ameliorating IL-1ra-L polypeptide-related disease, condition or disorder
 CC which include rheumatoid arthritis, psoriatic arthritis, inflammatory
 CC arthritis, osteoarthritis, autoimmune disease, multiple sclerosis,
 CC lupus, diabetes, transplant rejection, inflammatory joint disease, graft
 CC versus host disease and inflammatory conditions resulting from strain,
 CC sprain, cartilage damage, trauma, orthopaedic surgery, hepatitis, human
 CC immunodeficiency virus (HIV) infection, clostridium-associated
 CC diarrhoea, leprosy, pulmonary tuberculosis, septic shock, obesity,
 CC anorexia, myopathies, Alzheimer's disease, Parkinson's disease, memory,
 CC disorders, acute respiratory disease syndrome, cystic fibrosis, asthma,
 CC psoriasis, eczema, acute and chronic glomerulonephritis, osteoporosis,
 CC lymphomas, lung and breast cancer, leukaemias, infertility, endometriosis,
 CC endometriosis, retinal degeneration, retinal neuropathy, acute
 CC pancreatitis and Kawasaki's disease.
 XX SQ Sequence 273 AA:

Query Match 45.3%; Score 379; DB 22; Length 273;
 Best Local Similarity 48.3%; Pred. No. 6.8e-34;
 Matches 70; Conservative 30; Mismatches 45; Indels 0; Gaps 0;

QY 9 PTKSTAIROSROMWWLGSNLSIAPLRSRSTKPVTHIACRDTEESDKERGKMYWIGIK 68
 1: :|:|||:|||:|||:|||:|||:|||:|||:|||:
 125 pqrgsqidnhrwwlqdatliavrkdrmspvialiscrhvetslekdrgdpilgln 184

QY 69 KPKLFCABIQPLTQEKEKNIMDLYVERKAQPKPLFFHNKEGSTSVFOSVSYGWIA 128
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 185 hnicmcakvgdqptiqikekdmllyndpepkfiflyhsqsnstfesvalpgwfa 244

QY 129 TSTMGGQPFLTKERGITNNNFYL 153
 |: :|: ||: |: ||: |: ||: |:
 Db 245 vsseggcpiltqelgkantdfgl 269

RESULT 8
 AAW63136
 ID AAW63136 standard; Protein; 169 AA.
 XX
 AAW63136;
 AC AX
 DT 14-OCT-1998 (first entry)
 XX DE Interleukin-1 receptor antagonist beta (IL-1ra-beta).
 XX Interleukin-1 receptor antagonist beta; IL-1ra-beta; IL-1 alpha;
 KW IL-1 beta; inflammatory response; treatment; inflammation; septicaemia;
 KW cancer; anaemia; arthritis; inflammatory bowel disease; cardiac ischaemia;
 KW graft vs. host rejection; autoimmunity; stroke; restenosis;
 KW acute respiratory disease syndrome; psoriasis; resstenosis;
 KW traumatic brain injury; acquired immune deficiency syndrome;
 KW cachexia.
 XX OS Homo sapiens.
 XX PR EP855404-A1.
 XX PD 29-JUL-1998.
 XX PT WPI; 1998-389778/34.
 DR N-PSDB; AAV42659.
 XX PT New nucleic acid encoding human interleukin-1 receptor antagonist.
 PT beta polypeptides - and related expression systems, transformed
 PT cells, proteins, antibodies, agonists and antagonists, useful for
 PT treatment, prevention and diagnosis of inflammation, septicaemia,
 PT cancer etc
 XX PS Claim 13; FIG 2; 20pp; English.
 CC The present sequence represents human Interleukin-1 receptor antagonist
 CC beta (IL-1ra beta). IL-1 alpha and IL-1 beta play key roles in
 CC inflammatory responses, and are produced aszymogens which are cleaved
 CC upon secretion to yield mature carboxyl terminal 17 kb fragments.
 CC IL-1ra beta polypeptides and polynucleotides are useful in treatments of
 CC chronic and acute inflammation, septicæmia, cancer, anaemia, arthritis,
 CC inflammatory bowel disease, graft vs. host rejection, autoimmunity,
 CC stroke, cardiac ischaemia, acute respiratory disease syndrome (ARDS),
 CC psoriasis, restenosis, traumatic brain injury, acquired immune
 CC deficiency syndrome (AIDS) and cachexia. These conditions (or
 CC susceptibility to them) may be diagnosed by detecting mutations in the
 CC IL-1ra beta coding sequence analysing a sample for presence or amount
 CC of IL-1ra-beta.
 XX Sequence 169 AA;

Query Match 42.2%; Score 345.5; DB 19; Length 169;
 Best Local Similarity 45.0%; Pred. No. 1.9e-30;
 Matches 68; Conservative 29; Mismatches 53; Indels 1; Gaps 1;

QY 4 QREAAPKAYAIRSROMWWLGSNLSIAPLRSRSTKPVTHIACRDTEESDKERGKMY 63
 |: :|: ||: |: |||: |||: |||: |||: |||:
 Db 17 qsnckpigtindringqwtlqgnlvavrdsavtvpvavickyppeallegrggpy 76

molecules and their corresponding nucleic acid sequences, designated as interleukin-delta (IL-Delta) and interleukin-epsilon (IL-Epsilon). IL-Delta and IL-Epsilon are useful for treating conditions exhibiting abnormal expression of the interleukin such as immunological disorders, tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis, allergy, autoimmune diseases and infectious diseases (e.g., pulmonary tuberculosis, leprosy, fulminant hepatitis, and viral infections such as HTV). The invention also relates to methods of using the composition containing IL-Delta or IL-Epsilon for both diagnostic and therapeutic utilities. IL-Delta is used as an immunogen for the production of antisera or antibodies specific, e.g., capable of distinguishing between IL-1 family members and an IL-Delta, for the interleukin or its fragment. The purified interleukin is used as a reagent to detect any antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous cytokine. The invention also contemplates the use of competitive drug screening assays. The present sequence is human Interleukin-1epsilon (IL-Epsilon) protein.

PT synergistic treatment of interleukin (IL)-mediated diseases; useful for
 e.g. septic shock; comprises adjunctively administering IL-1 receptor
 antagonist polypeptide and non-steroidal IL-1 processing and release
 PT inhibiting agent -
 PS Disclosure; Page 91; 112pp; English.
 XX
 CC The present sequence is a human interleukin-1 receptor antagonist
 CC (IL-1ra). The present sequence or its variant may be administered
 CC in combination with a non-steroidal IL-1 processing and release
 CC inhibiting agent for the treatment or prevention of IL-mediated disease
 CC states. The composition is useful for treating inappropriate host
 CC responses to infectious diseases where active infection exists at any
 CC body site, e.g. septic shock; disseminated intravascular coagulation;
 CC inflammation due to antigen, antibody and/or complement deposition;
 CC inflammatory conditions including arthritis, cholangitis, colitis,
 CC encephalitis, endocarditis, glomerulonephritis, hepatitis, myocarditis,
 CC pancreatitis, pericarditis, and reperfusion injury vasculitis. It is
 CC also useful for treating immune based diseases including conditions
 CC involving T cells and/or macrophages e.g. acute and delayed
 CC hypersensitivity, graft rejection, graft-versus-host disease;
 CC autoimmune diseases including Type 1 diabetes mellitus and multiple
 CC sclerosis. The composition may be used for treating bone and cartilage
 CC resorption as well as diseases resulting in excess deposition of
 CC extracellular matrix. Such diseases include osteoporosis, periodontal
 CC diseases, interstitial pulmonary fibrosis, cirrhosis, systemic sclerosis
 CC and keloid formation. It is also useful for treating tumours which
 CC produce IL-1_a as an autocrine growth factor and for preventing the
 CC cachexia associated with certain tumours. It may be used for
 CC treating neuronal diseases with an inflammatory component e.g.
 CC Alzheimer's disease, stroke, depression and concussion injury and for
 CC cardiovascular diseases in which recruitment of monocytes into the
 CC subendothelial space plays a role, e.g. the development of
 CC atherosclerotic plaques.
 XX

SQ Sequence 169 AA:
 Query Match Best Local Similarity 42.2%; Score 345.5; DB 22; Length 169;
 Matches 68; Conservative 29; Mismatches 53; Indels 1; Gaps 1;
 Qy 4 OREAAPKSYAIRDSRQRMWVLGSNLSTIAPLSLRSRIKPYVTLHLACRDPEDFSDEKEGNMYY 63
 Db 17 qsmckpbtgtindinqwvltlqgqnivavprsdsvtpvtavtckyapealedgrgdly 76
 Qy 64 LGIKGKDLCIECAEIQCKPTLQLKERNIMDLVYVEKKAAQPKPFLEFHNKRGSTSVFQSVA 123
 Db 77 lgiqpmpcmlycqvgeqptiqkqeqmldyqgpewpkpflyraktrgststlesvafp 136
 Qy 124 GWFLIAATSTSGQPIFLKLRGTTNNNTNFYLD 154
 Db 137 dwflaasskrdqpiiltseigksyntafeln 166

RESULT 13
 AAB5001
 ID AAB5001 standard; protein; 130 AA.
 XX
 AC AAB5001;
 XX
 DT 06-AUG-2001 (first entry)
 DE Human interleukin-1 receptor antagonist (NCVINTRA C) polypeptide.
 XX
 KW transmembrane protein; NOVRAN; neuropeptide; NOVNUR;
 KW gonadotropin-like protein; NOVGON; interleukin-1; NOVINTRA; human;
 KW cytostatic; neuroprotective; reproductive; antiinflammatory; cancer;
 KW antibacterial; cerebroprotective; antidiabetic; antiarthritic;
 KW antiasthmatic; antiallergic.
 XX

XX WO200140291-A2.
 XX
 XX
 PD 07-JUN-2001.
 XX
 PR 06-DEC-2000; 2000WO-US33029.
 XX 06-DEC-1999; 99US-0169056.
 PR 05-DEC-1999; 99US-0169866.
 PR 09-DEC-1999; 99US-0169886.
 PR 10-DEC-1999; 99US-0170252.
 PR 12-JAN-2000; 2000US-0175740.
 PR 05-DEC-2000; 2000US-0170252.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Burgess CE, Prayaga SK, Shimkets RA, Rastelli L, Zerhusen BD;
 PI Mezes PS;
 XX WPI; 2001-374790/39.
 DR N-PSDB; AAFB38790.
 XX
 PT Novel isolated human transmembrane, neuromedin peptide antagonist
 PT gondotropin-like protein and interleukin-1 receptor antagonist
 PT metabolic function disorders -
 XX
 PS Claim 53; Fig 15B; 138pp; English.
 XX
 CC The invention provides novel polypeptides (NOVX) selected from human
 CC transmembrane protein (NOVTRN), neuromedin peptide (NOVNEUR),
 CC gonadotropin-like protein (NOVGN) and two interleukin-1 receptor
 CC antagonist proteins (NOVINTRA A and B). The invention also provides
 CC methods in which a NOVX polypeptide, polynucleotide and antibody are
 CC used in the detection, prevention and treatment of a broad range of
 CC pathological states. NOVINTRA can be used to treat a cell signaling
 CC disorder such as cancer, immune response disorder, hematopoietic
 CC disorder, neurodegenerative disorder. NOVNEUR can be used to treat
 CC endocrine disorder, muscle disorder, neurologic disorder, cancers of
 CC central nervous system, breast, colon, ovary, kidney, prostate and
 CC thyroid. NOVGN can be used to treat reproductive development disorder,
 CC metabolic function disorder and melanoma. NOVINTRA A and B can be used
 CC to treat bone metabolism or structure disorder, septic shock, diabetes,
 CC arthritis and cancer. The present sequence represents the NOVINTRA C
 CC
 XX Sequence 130 AA;
 SQ
 Query Match 42.2%; Score 345; DB 22; Length 130;
 Best Local Similarity 50.4%; Pred. No. 1_5e-30;
 Matches 66; Conservative 25; Mismatches 36; Indels 4; Gaps 2;
 QY 16 DSRQWVWLSGNSLAAPLRSKPTVHLACRDTESDKERGKGNMVGIRKDCLFC 75
 1 dihrwvwlqdgtilavp-ikvfpvtialscrhvetlekgdsgnpylglnlcm 58
 QY 76 AEGQGPTLOKR-ENIMDLVKEVKRQKPRPFHNGESTSYFQSYSPGNITATSTS 133
 59 avkgdptiqklqekalmldlyngpepvksfifysqsgnrfstfvalpawglavasseg 118
 QY 134 GQPFLTKERG 144
 Db 119 gcpilntqelg 129
 SQ Sequence 208 AA;
 RESULT 14
 ID AAY24044
 XX Standard; Protein: 208 AA.
 AC AAY24044;
 XX
 XX 30-SEP-1999 (first entry)
 XX DE A human SPOIL-II protein (also known as htANGO 080-II).
 XX SPOL-II; interleukin-1 receptor antagonist; IL-1ra; modulating agent;
 KW bone metabolism disorder; proinflammatory disorder; immune disorder;
 KW inflammatory disease; septic shock; stroke; diabetes; arthritis;
 KW intercolitis; pneumonitis; epithelial cell; skin disease;
 KW proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;
 KW epithelial cancer; squamous cell carcinoma; bone resorption disorder;
 KW osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;
 KW osteogenesis imperfecta; fibrous dysplasia; hypophosphatasia;
 KW bone sarcoma; myeloma; bone disorder; osteolytic bone lesion;
 KW hypercalcemia; bone mass; bone fragility; bone pain; bone deformity;
 KW bone fracture; htANGO 80-I.
 XX OS Homo sapiens.
 XX FH Location/Qualifiers
 FT 98..724
 FT /tag= a
 FT /product= SPOIL-II
 XX WO9937662-A1.
 XX PD 29-JUL-1999.
 XX PF 26-JAN-1999; 99WO-US01575.
 XX PR 27-JAN-1998; 98US-0013910.
 XX PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 XX PI Busfield SJ;
 XX FS WPI; 1999-458675/38.
 DR N-PSDB; AAX86459.
 XX
 PT New isolated SPOIL Proteins, used to develop products for treating,
 PT e.g. inflammatory and immune disorders
 XX
 FS Claim 8; Fig 5; 126pp; English.
 XX
 CC The present sequence represents a SPOIL-II protein. SPOIL proteins have
 CC homology to interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.
 CC The SPOIL proteins are used as modulating agents in regulating a variety
 CC of cellular processes. The products can be used for treating disorders
 CC characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone
 CC metabolism disorder, a proinflammatory disorder or an immune disorder.
 CC They can be used for treating e.g. inflammatory diseases and disorders
 CC e.g. inflammation, septic shock, stroke, diabetes, arthritis, and/or skin diseases and
 CC intercolitis and pneumonia. epithelial cell and/or skin diseases and
 CC disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma
 CC and Kaposi's sarcoma and other epithelial cancers including squamous cell
 CC carcinoma, oesophageal cancer and cancer of the mouth and/or throat); and
 CC bone-related and/or bone resorption disorders (e.g. osteoporosis, Paget's
 CC disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,
 CC fibrous dysplasia, hypophosphatasia, bone sarcoma, myeloma, bone disorder
 CC (e.g. osteolytic bone lesions) and hypercalcemia. SPOIL molecules and
 CC SPOIL modulators are useful for regulation of bone mass (e.g. increase in
 CC bone mass and/or inhibit bone loss), management of bone fragility (e.g.
 CC decrease bone fragility); and prevention and/or treatment of bone pain,
 CC bone deformities and/or bone fractures. The products can also be used for
 CC detection, diagnosis and screening assays.
 XX
 Query Match 42.1%; Score 344.5; DB 20; Length 208;
 Best Local Similarity 45.9%; Pred. No. 3_2e-30;
 Matches 67; Conservative 29; Mismatches 49; Indels 1; Gaps 1;
 QY 9 PKSYAIRDSRQWVWLSGNSLAAPLRSKPTVHLACRDTESDKERGKGNMVGIRK 68

RESULT 15
 Db 61 pitgtindinqwvtllggqnlavprsdsvptvavtckyrealedgrgdpvlgln 120
 Qy 69 KDCICFCAEIQGKPTIQLKEKNIMDLIVKEKKQKPLFHNKEGSTV 128
 Db 121 PemcIycckgeqptlqikekimidlyqgpepvkpflyrakrgtstlesvpfdwfia 180
 Qy 129 TSTRSGQPIFLTKERGTTNNTFYLD 154
 Db 181 sskrd-qpiiltselgksyntafeln 205

Search completed: May 10, 2002, 09:11:45
 Job time: 115 sec

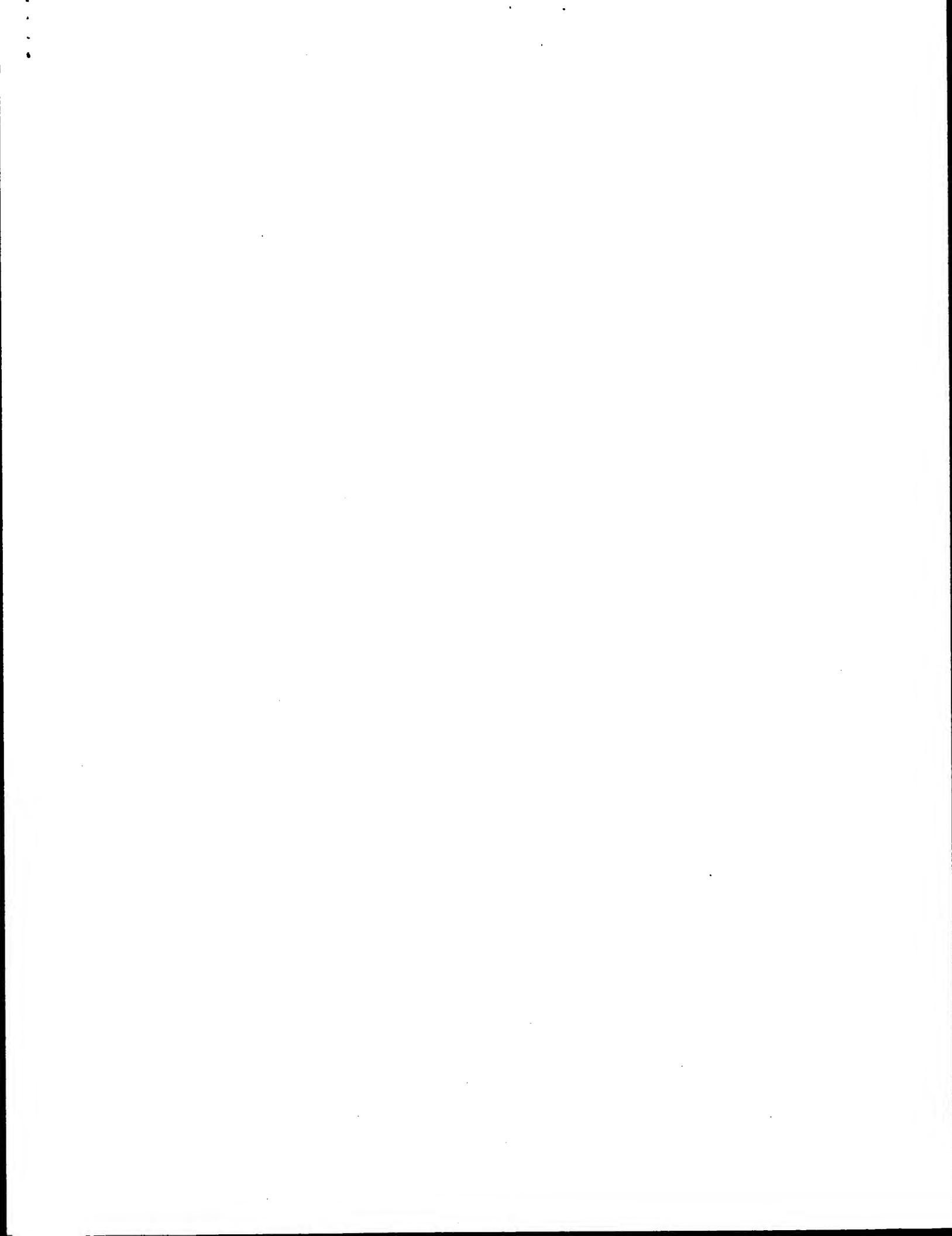
Db 1 mnkekkelraaspslrhvqdlsrrvwilqnultavprkeqvptitllpcqyltdtlen 60
 Qy 58 KGNNVYLGJGKDKDCLFCAEIQGKPTIQLKEKNIMDLIVKEKKQKPLFHNKEGSTV 117
 Db 61 rgdptymgvqrpmascifctkdgepvlqggnemynkkpvrkaslfyfksgstsf 120
 Qy 118 QSYSPGMATSTSGQPIFLTKERGTTNNTNF 151
 Db 121 esaafpgftiaveskgsclpiltdgelgeifitdf 154

RESULT 15
 AAWB6286
 ID AAWB6286 standard; Protein: 160 AA.
 XX
 AC AAWB6286;
 XX
 DT 19-FEB-1999 (first entry)
 DE Rodent interleukin (IL)-1 epsilon polypeptide.
 XX
 KW Interleukin; IL-1 delta; polyclonal antibody; IL-1 epsilon; cytokine;
 KW inflammatory response; immune system; diagnosis; agonist; antagonist;
 KW chemokine.
 OS Mus sp.
 XX
 PN WO9847921-A1.
 XX
 PD 29-OCT-1998.
 XX
 PF 17-APR-1998; 98W0-US06879.
 XX
 PR 06-AUG-1997; 97US-0055111.
 PR 21-APR-1997; 97US-0837627.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 PI Bazan JF, Hedrick JA, Kastelein RA, Sana TR;
 XX
 DR WPI; 1998-609976/51.
 DR NPSDB; AAV71960.
 XX
 PT Mammalian interleukin 1-delta and 1-epsilon - useful for, e.g.
 PT regulating the immune system and inflammatory responses
 XX
 PS C1.aim 1; Pages 92-93; 113pp; English.
 XX
 CC This represents a rodent interleukin (IL)-1 epsilon polypeptide. The
 CC invention relates to a recombinant polypeptide that specifically binds
 CC polyclonal antibodies (Abs) generated against a 12 consecutive amino acid
 CC segment of IL-1 delta or IL-1 epsilon. Agonists or antagonists of these
 CC polypeptides are used to regulate a cell involved in an inflammatory
 CC response. The IL-1 delta or IL-1 epsilon polypeptides and peptides are
 CC used to produce Abs and antigen-Ab complexes. The polypeptides, Abs and
 CC the corresponding nucleic acids regulate development and/or the immune
 CC system, and can be used to diagnose and treat conditions associated with
 CC abnormal expression of IL. Agonists or antagonists of IL-1 delta or IL-1
 CC epsilon polypeptides are used with agonists or antagonists of IL-1 alpha,
 CC IL-1RA, IL-1L gamma, IL-2 and/or IL-12. The IL-1 delta or IL-1
 CC epsilon polypeptides may be used as a soluble polypeptide or as a fusion
 CC protein with another cytokine or chemokine.
 XX
 SQ Sequence 160 AA;

Query Match 35.9%; Score 293.5; DB 19; Length 160;
 Best Local Similarity 37.7%; Pred. No. 1e-24;
 Matches 58; Conservative 31; Mismatches 62; Indels 3; Gaps 1;
 Qy 1 MNPQE--AAPKSAYAIRDSRQMVWLGSNSLIAPLRSRIKPVHLIACRDTESDKE 57
 || ::|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :

Tue May 14 08:26:36 2002

us-09-723-676-2.rag



R; Elsenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson, Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A; Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family:
A; Reference number: A40956; MUID:91271363
A; Molecule type: DNA
A; Residues: 7-178 <ETS>
A; Cross-references: GB:M63100; NID:9198389; PIDN:AAA393101; PID:9198390
R; Shuck, M.E.; Bassau, T.E.; Tracey, D.E.; Bienkowski, M.J.
Eur. J. Immunol. 21, 2775-2780, 1991
A; Title: Cloning, heterologous expression and characterization of murine interleukin 1
A; Reference number: A49031; MUID:92037824
A; Accession: A49031
A; Molecule type: mRNA
A; Residues: 23-178 <SHU>
A; Cross-references: GB:S64082; NID:9238584; PIDN:AAB20265_1; PID:9238585
A; Experimental source: peritoneal macrophages, ICR strain
A; Note: sequence extracted from NCBI backbone (NCBIN64082; NCBIPI:6085)
R; Zahedi, K.; Seidlin, M.F.; Rits, M.; Ezekowitz, R.B.; Whitehead, A.S.
J. Immunol. 146, 4228-4233, 1991
A; Title: Mouse IL-1 receptor antagonist protein: Molecular characterization, gene mapping
A; Reference number: 156106; MUID:91250712
A; Accession: 156106
A; Status: preliminary; translated from GB/EMBL/DDJB
A; Molecule type: mRNA
A; Residues: 1-178 <RES>
A; Cross-references: GB:M74294; NID:9198387; PIDN:AAA39309_1; PID:9198388
R; Zahedi, K.A.; Uhlar, C.M.; Rits, M.; Prada, A.E.; Whitehead, A.S.
Cytokine 6, 1-9, 1994
A; Title: The mouse interleukin 1 receptor antagonist protein: gene structure and regulation
A; Reference number: 152970; MUID:94271931
A; Accession: 152970
A; Status: preliminary; translated from GB/EMBL/DDJB
A; Molecule type: DNA
A; Residues: 1-178 <RE2>
A; Cross-references : GB:L32838; NID:91487864; PIDN:AAA20575_1; PID:95288978
A; Gene: IL-1rn
A; Introns: 40/2; 70/1; 107/3
C; Superfamily: interleukin-1
C; Keywords: cytokine receptor
F1-26/Domain: signal sequence #status predicted <SIG>
F1-27-178/Product: interleukin-1 receptor antagonist #status predicted <MA2>
Query Match 23, 9%; Score 195.5; DB 2; Length 178;
Best Local Similarity 33.6%; Pred. No. 4.1e-12;
Matches 49; Conservative 23; Mismatches 49; Indels 25; Gaps 3;
C; Species: Homo sapiens (man)
C; Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 26-May-2000
C; Accession: A40956; I37894; A30568; S08160; S08159; A37822
R; Elsenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson, Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A; Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family:
A; Reference number: A40956; MUID:91271363
A; Accession: A40956
A; Molecule type: DNA
A; Residues: 1-177 <EIS>
A; Cross-references: GB:M63099; NID:9186385; PIDN:AAB41943_1; PID:9186386
R; Lennard, A.; Gorman, P.; Carrier, M.; Griffiths, S.; Scotney, H.; Sneer, D.; Solari, Cytokine 4, 83-89, 1992
A; Title: Cloning and chromosome mapping of the human interleukin-1 receptor antagonist
A; Reference number: 137894; MUID:92338323
A; Accession: 137894
A; Status: translated from GB/EMBL/DDJB
A; Molecule type: DNA
A; Residues: 1-177 <LEN>
A; Cross-references: EMBL:X64532; NID:933798; PIDN:CAA45832_1; PID:933799
R; Carrier, D.B.; Deibel Jr., M.R.; Dunn, C.J.; Tomich, C.S.C.; Laborde, A.L.; Slightom, L.G.; Sieu, L.C.; Hardie, M.M.; Zurched-Neely, H.A.; Reardon, I.M.; Heinrikson, R.L.; Nature 344, 633-638, 1990
A; Title: Purification, cloning, expression and biological characterization of an interleukin-1 receptor
A; Reference number: A30368; MUID:90220867
A; Accession: A30368
A; Molecule type: mRNA
A; Residues: 1-177 <CAR>
A; Cross-references: GB:X53296; NID:922578; PIDN:CAA37386_1; PID:932579
A; Note: parts of this sequence, including the amino end of the mature protein, were c
R; Elsenberg, S.P.; Evans, R.J.; Arend, W.P.; Verderber, E.; Brewer, M.T.; Hannum, C.H
Nature 343, 341-346, 1990
A; Title: Primary structure and functional expression from complementary DNA of a human interleukin-1 receptor antagonist precursor - rat
A; Reference number: S08160; MUID:90136921
A; Accession: S08160
A; Status: not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-177 <EL2>
A; Cross-references: GB:X52015; NID:922576; PIDN:CAA6262_1; PID:932577
R; Hannum, C.H.; Wilcox, C.J.; Arend, W.P.; Joslin, F.G.; Driggs, D.J.; Heimdal, P.L.; Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Thompson, C.; Reference number: A40956; MUID:91271363
A; Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family:
A; Reference number: A40956; MUID:91271363
A; Accession: C40956

RESULT 4

A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-178 <EIS>
A; Cross-references: GB:M63101; NID:9204928; PIDN:AAA41434_1; PID:9204929
C; Superfamily: interleukin-1
C; Keywords: cytokine receptor

Query	Match	Score	DB	Length
QY	4 QREAAPKSAIRDSRQMVWLSGNSLIA--APLSRSKPVTLHLIACRDTESDKEKG 59	22.4%	2	178
Db	31 KRCKMQAFRRIWDINQKTYFLRNNOILAGIQLGPVKLERKDMVIFDRN----- 81	31.9%	11	178
QY	60 NMVYLGIKGKDKLCIFCAEGQKPTIQLEKEENIMDVYEKAQKPELFHHNRKGESTSYFOS 119	31.9%	11	178
Db	82 -VFLGIHGKLSCVSGDDTKLQLEEVNTDLNKNKEEDKRFIFIRSETGPTTSES 139	31.9%	11	178
QY	120 VSYPGWFIASTTSQGPILF 140	31.9%	11	178
Db	140 LACPGFWFLCTTLEADHPVSLT 160	31.9%	11	178

Query Match 22.4%; Score 183.5; DB 2; Length 178;
Best Local Similarity 31.9%; Pred. No. 5.4e-11;
Matches 45; Conservative 26; Mismatches 55; Index 15; Gaps 2;

A;Residues: 26-75;97-108;110-116;120-111;163-176 <HAN>
 R;Bielenkowski, M.J.; Bessalou, T.E.; Berger, A.E.; Truesdell, S.E.; Shelly, J.A.; Laborde,
 J.; Biol. Chem. 265: 14505-14511; 1990
 A;Title: purification and characterization of interleukin 1 receptor level antagonist pr
 A;Reference number: A37822; MUID:90354444
 A;Molecule type: protein
 A;Residues: 26-52;10-77;122-127;170-175 <BIE>
 A;Experimental source: culture medium, PMA-stimulated THP-1 cells
 C;Comment: For an alternative splice form, see PIR:A39386
 C;Genetics:
 C;Keywords: alternative splicing; cytokine receptor; extracellular protein; glycoprotein
 F;1-25/Domain: signal sequence #status predicted <SG>
 F;26-177/Product: interleukin-1 receptor antagonist #status experimental <MAT>
 F;26-177/Product: interleukin-1 receptor antagonist #status covalent) #status experimental
 F;109/Binding site: carbohydrate (Asn) (covalent)
 RESULT 5

Query Match 22.2%; Score 182; DB 2; Length 177;
 Best Local Similarity 27.9%; Pred. No. 8 9e-11;
 Matches 46; Conservative 27; Mismatches 64; Indels 28; Gaps 4;
 QY 4 OREAAPKSYAIRDSDRQMVWLSGNSLIAPLSR-----SIKVTLHIACTEFS 54
 QY ::::|::|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 30 RKSSKMQAFRIWDVNQTKTFYLRRNQLVAGYLOGPNWNLNEEKIDVVPVIEPHAL----- 81
 QY 55 DKEKGNNMYLGIKGKDLCIFCAEQGKPLQLKEKNIMDLYVEKKAKQPKPFFFHNKEGST 114
 QY ::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 82 -----FGLHGKRMCLSCVKSGBTRQLAEVNITDLSENRKDRFAFIRSQPT 133
 QY 115 SVFOSVSYPGFIATSTSGQPFLTK--ERGITINNTNFYLDSE 157
 QY :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 134 TSFESAACPGWFCLTAMEADQPVSLTNMPDEGVM-VTKFYFOEDE 177

RESULT 5

A39386
 Interleukin-1 receptor antagonist, long intracellular splice form - human
 N;Contains: interleukin-1 receptor antagonist, short intracellular splice form
 C;Species: Homo sapiens (man)
 C;Date: 28-Feb-1992 #sequence_revision 11-Apr-1997 #text_change 26-May-2000
 C;Accession: A39386
 R;Muñoz, M.; Polentanutt, N.; Sironi, M.; Poli, G.; De Gioia, L.; Introna, M.; Mantovani,
 J. EXP. Med. 182, 623-628, 1995
 A;Title: Cloning and characterization of a new isoform of the interleukin 1 receptor ant
 A;Reference number: 137893; MUID:95355865
 A;Status: translated from GB/EMBL/DDBJ
 A;Residues: 1-180 <RES>
 A;Cross-references: EMBL:XA4348; NID:91009970; PIDN:CAA59087.1; PID:91009971
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Accession: A39386
 A;Residues: 1-180 <RES>
 A;Cross-references: EMBL:XA4348; NID:91009970; PIDN:CAA59087.1; PID:91009971
 R;Haskill, S.; Martin, G.; Van Le, L.; Morris, J.; Peace, A.; Bigler, C.F.; Jaffe, G.J.;
 Proc. Natl. Acad. Sci. U.S.A. 88, 3681-3685, 1991
 A;Title: cDNA cloning of an intracellular form of the human interleukin 1 receptor antag
 A;Reference number: A39386; MUID:91219436
 A;Accession: A39386
 A;Molecule type: mRNA
 A;Residues: 1-3-25-180 <HAS>
 A;Cross-references: GB:M55446; NID:9186291; PIDN:AAA59138.1; PID:9186292
 C;Comment: For an alternative splice form, see PIR:A30368
 C;Genetics:
 A;Gene: GDB:ILRN
 A;Cross-references: GDB:125897; OMIM:147679
 A;Map position: 2q14.2-2q14.2
 C;Superfamily: interleukin-1
 C;Keywords: alternative splicing; cytokine receptor
 F;1-180/Product: interleukin-1 receptor antagonist, long intracellular splice form #stat
 F;1-3,25-180/Product: interleukin-1 receptor antagonist, short intracellular splice form

RESULT 6

A54377
 Interleukin-1 receptor antagonist secreted form precursor - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 06-oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
 C;Accession: A54377; I46729
 R;Cominelli, F.; Bortolami, M.; Piarro, T.T.; Monsacchi, L.; Ferretti, M.; Brewer, M.
 J. Biol. Chem. 269, 6962-6971, 1994
 A;Title: Rabbit interleukin-1 receptor antagonist. Cloning, expression, functional ch
 A;Reference number: A54377; MUID:94165101
 A;Molecule type: mRNA
 A;Residues: 1-177 <CON>
 A;Cross-references: GB:S88977; NID:9545740; PIDN:AA830993.1; PID:9545741
 A;Experimental source: colon tissue
 A;Note: sequence extracted from NCBI backbone (NCBN:14168, NCBI:14169)
 R;Goto, F.; Goto, T.; Miyata, T.; Ohkawa, S.; Takao, T.; Mori, S.; Furukawa, S.; Ma
 Immunology 77, 235-244, 1992
 A;Title: Interleukin-1 receptor antagonist in inflammatory exudate cells of rabbits. P
 A;Reference number: 146729; MUID:9052512
 A;Accession: I46729
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-177 <GOT>
 A;Cross-references: GB:D21832; NID:9425787; PIDN:BA04860.1; PID:9452205
 C;Species: Homo sapiens (man)
 C;Date: 28-Feb-1992 #sequence_revision 11-Apr-1997 #text_change 26-May-2000
 C;Accession: A39386
 A;Title: Cloning and characterization of a new isoform of the interleukin 1 receptor ant
 A;Reference number: 137893; MUID:95355865
 A;Status: translated from GB/EMBL/DDBJ
 A;Residues: 1-180 <RES>
 A;Cross-references: EMBL:XA4348; NID:91009970; PIDN:CAA59087.1; PID:91009971
 R;Haskill, S.; Martin, G.; Van Le, L.; Morris, J.; Peace, A.; Bigler, C.F.; Jaffe, G.J.;
 Proc. Natl. Acad. Sci. U.S.A. 88, 3681-3685, 1991
 A;Title: cDNA cloning of an intracellular form of the human interleukin 1 receptor antag
 A;Reference number: A39386; MUID:91219436
 A;Accession: A39386
 A;Molecule type: mRNA
 A;Residues: 1-3-25-180 <HAS>
 A;Cross-references: GB:M55446; NID:9186291; PIDN:AAA59138.1; PID:9186292
 C;Comment: For an alternative splice form, see PIR:A30368
 C;Genetics:
 A;Gene: GDB:ILRN
 A;Cross-references: GDB:125897; OMIM:147679
 A;Map position: 2q14.2-2q14.2
 C;Superfamily: interleukin-1
 C;Keywords: alternative splicing; cytokine receptor
 F;1-180/Product: interleukin-1 receptor antagonist, long intracellular splice form #stat
 F;1-3,25-180/Product: interleukin-1 receptor antagonist, short intracellular splice form

RESULT 7

ICBO1B
 Interleukin-1 beta Precursor - bovine
 N;Alternative names: hematopoietin-1; IL-1 beta
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999
 C;Accession: JL0010; S01380

A;Residues: 1-269 <MAR>
A;Cross-references: GB:X02532; NID:933789; PIDN:CAA26372.1; PID:933790
A;Note: parts of this sequence, including the amino end of the mature form, were confirmed by Webb, A.C.; DiMarella, C.A.; Rosenwasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Au, Adv. Gene Technol., 22, 339-340, 1985
A;Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
A;Reference number: 151852
A;Accession: 151852
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-5, 'K', 7-19, 'H', 21-110, 'Q', 112-176, 'A', 178-213, 'P', 215-269 <WEBB>
A;Cross-references: GB:M54933; NID:9186287; PIDN:AAA59136.1; PID:9186288
A;Title: cDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell line.
A;Reference number: 152217; MUID:87156769
A;Accession: 165200
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-269 <NTS>
A;Cross-references: GB:M15330; NID:9186283; PIDN:AAA59135.1; PID:9307045
R;Kotenko, S.V.; Bulentov, M.T.; Veiko, V.P.; Epishin, S.M.; Lomakin, I.B.; Emel'yanov, I.I.; Vinetskii, Y.P.
Dokl. Akad. Nauk SSSR 309, 1005-1008, 1989
A;Title: Cloning of the cDNA coding for human prointerleukin-1 alpha and prointerleukin-1 beta.
A;Reference number: 138131; MUID:90249285
A;Accession: 138132
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residue: 1-269 <KOT>
A;Cross-references: EMBL:X56087; NID:935662; PIDN:CAA39567.1; PID:935663
R;Zsebo, K.M.; Wypych, J.; Yuschenko, V.N.; Lu, H.; Hunt, P.P.; Langley, K.
Blood 71, 962-968, 1988
A;Title: Effects of hematopoietin-1 and interleukin 1 activities on early hematopoietic
A;Reference number: A90732; MUID:88184226
A;Accession: B27616
A;Molecule type: protein
A;Residue: 117-123, 'X', 125-126, 'X', 128 <ZSE>
R;Stevenson, F.T.; Bursten, S.L.; Fanton, C.; Locksley, R.M.; Lovett, D.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 7245-7249, 1993
A;Title: The 31-kDa precursor of interleukin 1alpha is myristoylated on specific lysines
A;Reference number: A48933; MUID:93348250
A;Contents: annotation: myristylation of lysines
R;Nanduri, V.B.; Rulmes, J.; Pan, Y.C.E.; Kilian, P.L.; Stern, A.S.
Biochim. Biophys. Acta 1118, 25-35, 1991
A;Title: The role of arginine residues in interleukin 1 receptor binding.
A;Reference number: S19608; MUID:92110334
A;Contents: annotation: type I IL-1 receptor interaction site
A;Note: modification of Arg-120 by phenylglyoxal blocks receptor binding
R;Clore, G.M.; Gronenborn, A.M.
submitted to the Brookhaven Protein Data Bank, January 1991
A;Reference number: A50049; PDB:61B
A;Contents: annotation: conformation by (13)C- and (1)H-NMR, residues 117-269
R;Clore, G.M.; Wingfield, P.T.; Gronenborn, A.M.
Biochemistry 30, 2315-2323, 1991
A;Title: High-resolution three-dimensional structure of interleukin 1beta in solution by
A;Reference number: A44675; MUID:91159409
A;Contents: annotation: (1)H-NMR structural determination
R;Hazuda, D.J.; Strickler, J.; Simon, P.; Young, P.R.
J. Biol. Chem. 266, 7081-7086, 1991
A;Title: Structure-function mapping of interleukin 1 precursors. Cleavage leads to a core
A;Reference number: A39774; MUID:91201363
A;Contents: annotation
J. Biol. Chem. 266, 7081-7086, 1991
A;Title: Structure-function mapping of interleukin 1 precursors. Cleavage leads to a core
A;Reference number: A50016, PDB:1IB
A;Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 119-269
R;Finzel, B.C.; Clancy, L.L.; Holland, D.R.; Muchmore, S.W.; Watengaugh, K.D.; Einspahr, J. Mol. Biol. 209, 779-791, 1989
A;Title: Crystal structure of recombinant human interleukin-1beta at 2.0 angstrom resolution
A;Reference number: A44666; MUID:9064532
A;Contents: annotation; X-ray crystallography, 2.0 angstroms
C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavage form of interleukin-1beta, unlike interleukin-1-alpha, is inactive.

ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.

C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin 1-alpha.

C;Genetics:

A;Gene: GDB:IL1B

A;Cross-references: GDB:120094; OMIM:147720

A;Map position: 2q13-2q21

A;Introns: 16/2; 33/3; 101/1; 156/1; 199/3

C;Superfamily: interleukin-1

C;Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macroparticle; myristate (Lys) (covalent) (partial) #status absent

F117-269/Product: interleukin-1 beta #status experimental

F176/Binding site: carbohydrate (Asn) (covalent) #status absent

F123/Binding site: carbohydrate (Asn) (covalent)

Query Match 20.0%; Score 163.5; DB 1; Length 269;
Best Local Similarity 33.1%; Pred. No. 1e-08;
Matches 52; Conservative 23; Mismatches 53; Indels 29; Gaps 6;

QY 14 IRDSRQMVWLLSSLNLIAPLRSIKPVYLHLIACRDTF-----FSDKEKN--IV 62
:|||:|| :|||:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 126 LRDSQQKSLVMSGPYELKA-----LHLQG-QDMHQOQVVSMSFVQGEESNDKIPV 174
QY 63 YLGTKGKDLCLFFAEIQLGKPTLQIKE--KNNMDLVKEKKAKPLFFHNKEGSTVFQS 119
:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 175 ALGKEKKNYLSCVLKDRLKPTLQIESDPKN---YPKRMKMEKRFVNKTIEINKLEFES 230
QY 120 VSYPGWFATSTTSQGPIPLTKEGRITNNNFYLDV 156
:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 231 AQFPNWKYSTSAENMPVFLGGKGQDITDFMFOV 267

RESULT 10

JN0724 interleukin-1 beta precursor - Pig
NID:Alternate names: hematopoietin-1; IL-1 beta
C;Species: Sus scrofa domesticus (domestic pig)

C;Accession: 14-JUL-1994 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999

R;Huetter, M.J.; Lin, G.; Smith, D.M.; Murtaugh, M.P.; Molitor, T.W.
Gene 129, 285-289, 1993

A;Title: Cloning, sequencing and regulation of an mRNA encoding porcine interleukin-1
A;Reference number: JN0724; MUID:93314975

A;Accession: JN0724

A;Molecule type: mRNA

A;Residues: 1-267 <HUE>

A;Cross-references: GB:M86725; NID:9164607; PIDN:AAA02584.1; PID:9164608

A;Experimental source: alveolar macrophage

C;Comment: This protein is a pleiotropic cytokine that mediates a variety of processes

C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavage form of interleukin-1beta, unlike interleukin-1-alpha, is inactive.

C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin 1-alpha.

C;Superfamily: interleukin-1

C;Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macroparticle; myristate (Lys) (covalent) #status predicted

F115-267/Product: interleukin-1 beta #status predicted

F177/Binding site: myristate (Lys) (covalent) #status predicted

Query Match 19.4%; Score 158.5; DB 1; Length 267;
Best Local Similarity 29.1%; Pred. No. 3.2e-08;
Matches 44; Conservative 28; Mismatches 58; Indels 21; Gaps 4;

QY 14 IRDSRQMVWLLSSLNLIAPLRSIKPVYLHLIACRDTF-----FSDKEKN--IV 63
:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 124 LDQDKHKSLSLAGPHMKA-----LHLTGLKREWVFCHSVQGDNSNNKIPV 173
QY 64 LGIGKGDCLFCAFIQLGKPTLQIKEKNMDLVKEKKAKPLFFHNKEGSTVFQS 123
:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 174 LGIGKGNLYLVCVMKDNTPTLQLED-PKRYPDRMEKRFVYKEVKRNVEFESALY 232
QY 124 GWFTATSTSGQPLTKERGITNNNFYLDV 154
:|||:|||:|||:|||:|||:|||:|||:|||:
Db 233 NWLFTSTSQAEQKPVFLGNNSKGQDITDFM 263

S38373	C;Species: Sus scrofa domestica (domestic pig)	Query Match 19.4%; Score 158.5%; DB 1; Length 268;
	C;Date: 20-May-1994 #sequence_revision 01-Dec-1995 #text_change 16-Jul-1999	Best Local Similarity 31.4%; Pred. No. 3.2e-08;
	C;Accession: S38373	Matches 48; Conservative 25; Mismatches 59; Indels 21; Gaps 4;
R;Vandenbroucke, K.; Fitten, P.; Beuken, E.; Martens, E.; Janssen, A.; van Damme, J.; Opde	QY 14 IRDSRQMWWLWSGNSLIAAPLSRSIKPVTLHLA-----CDTEFSDEKEGN--MYY 63	
Eur. J. Biochem. 217, 45-52, 1993	Db 125 LQDAQOKSLVLSGTYELKA-----LHLNAENLNQQVWVMSFVQGEESNDKIPV 174	
A;Title: Gene sequence, cDNA construction, expression in Escherichia coli and geneticall	QY 64 LGIKGKDLCLFCAEICKPTQLKEKNIMDLVVEKKAQKPFELFHNKKGSTSIVQSVP 123	
A;Reference number: S38373; MUID:94039070	Db 175 LGLRGRNLVUSCVMKDCKPTQLESDV-PNRPKKMEKRFVENKIEKDKEFESAQP 233	
A;Status: preliminary	QY 124 GWFIATSTTSQPIFLTKERGTINNTNFYLD 156	
A;Molecule type: DNA	Db 234 NWYIISITSQTEVMPVFLGNNSGGQDLDIFSMEV 266	
A;Residues: 1-267 <VAN>		
A;Cross-references: EMBL:X74568; NID:9407899; PIDN:CAA52660.1; PID:g407900		
C;Genetics:		
A;Introns: 16/2; 33/3; 99/1; 154/1; 197/3		
C;Superfamily: interleukin-1		
RESULT 12		
A30584	Query Match 19.4%; Score 158.5%; DB 2; Length 267;	
N;Best Local Similarity 28.4%; Pred. No. 3.2e-08;	Matches 42; Conservative 30; Mismatches 61; Indels 15; Gaps 4;	
N;Matches 42; Conservative 30; Mismatches 61; Indels 15; Gaps 4;		
QY 14 IRDSRQMWWLWSGNSLIAAPLSRSIKPVTLHLA-----CDTEFSDEKEGN--MYY 63		
:: : : : : : : : : : : : :		
Db 124 LQDKDEKALLVLAGPHFELKAHLKGDLLKREV----VFCMFSVQGDDSDDKIPVTGLI 176		
QY 67 KGKDLCLFCAEICKPTQLKEKNIMDLVVEKKAQKPFELFHNKKGSTSIVQSVP 126		
:: : : : : : : : : : : : :		
Db 177 KGKNLYLSCVMKDPTQLESDV-PNRPKKMEKRFVENKIEKDKEFESAQP 235		
QY 127 IATSTTSQPIFLTKERGTINNTNFYLD 154		
:: : : : : : : : : : : :		
Db 236 ISTSQABQPKPVFLGNNSKGQRDIDFTME 263		
RESULT 13		
A30584	Query Match 19.4%; Score 158.5%; DB 2; Length 267;	
N;Best Local Similarity 28.4%; Pred. No. 3.2e-08;	Matches 42; Conservative 30; Mismatches 61; Indels 15; Gaps 4;	
N;Matches 42; Conservative 30; Mismatches 61; Indels 15; Gaps 4;		
QY 14 IRDSRQMWWLWSGNSLIAAPLSRSIKPVTLHLA-----CDTEFSDEKEGN--MYY 63		
:: : : : : : : : : : : : :		
C;Species: Mus musculus (house mouse)		
C;Date: 26-Jul-1996 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999		
C;Accession: A27714; A30584; JU0082; A32166		
R;Mori, S.; Goto, F.; Goto, K.; Okawara, S.; Medea, S.; Shimada, K.; Yoshinaga, M.		
J. Immunol. 137, 3644-3649, 1986		
A;Title: Two interleukin 1 genes in the mouse: cloning and expression of the cDNA for one		
A;Reference number: 155969; MUID:87058957		
A;Status: preliminary; translated from GB/EMBL/DDBJ		
A;Molecule type: mRNA		
A;Residues: 1-269 <REBS>		
A;Cross-references: GB:MI5131; NID:9198293; PIDN:AAA39276.1; PID:g309398		
R;Telford, J.L.; Macchia, G.; Massone, A.; Carinci, V.; Palla, E.; Mellì, M.		
Nucleic Acids Res. 14, 9355-9963, 1986		
A;Title: The murine interleukin 1-beta gene: structure and evolution.		
A;Reference number: A24719; MUID:87117546		
A;Accession: A24719		
A;Molecule type: mRNA		
A;Residues: 1-269 <TEL>		
A;Cross-references: GB:X04964; NID:952666; PIDN:CAA28637.1; PID:g52667		
R;DeDomy, G.O.; Wilder, C.L.; Merenda, J.M.; McColl, A.S.; Geoghegan, K.F.; Otterness, F.B.; FEBs Lett. 278, 91-102, 1991		
A;Title: Reduction of biological activity of murine recombinant interleukin-1beta by a truncated form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.		
A;Reference number: S13029; MUID:91130610		
A;Accession: S13029		
A;Status: preliminary		
A;Molecule type: protein		
A;Residues: 1-18-269 <DAU>		
C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavage of the precursor is less heavily myristoylated than interleukin-1alpha.		
C;Genetics:		
C;Superfamily: interleukin-1beta		
C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen		
F;118-269/Product: interleukin-1 beta #status experimental <IL1>		
Query Match 19.3%; Score 158; DB 1; Length 269;		
Best Local Similarity 32.3%; Pred. No. 3.6e-08;		
Matches 50; Conservative 21; Mismatches 62; Indels 22; Gaps 5;		
QY 12 YAIIDSROMWWLWSGNSLIAAPLSRSIKPVTLHLA-----DTEFSDEKEGN--M 61		
:: : : : : : : : : : : :		
Db 125 YRLRDEQQKSLVLSDPYELKA-----LHLNGONTINOQVIFSMSVQGPSPNDKIP 174		
QY 62 WYLGIKGKDLCLFCAEICKPTQLKEKNIMDLVVEKKAQKPFELFHNKKGSTSIVQSVS 121		
:: : : : : : : : : : :		
Db 175 WAIGIIGKDLCLFCAEICKPTQLKEKNIMDLVVEKKAQKPFELFHNKKGSTSIVQSVP 233		

Qy 122 YPGWFIATSTSGOPILFTRKERRQTNINFLDSV 156
 :| :||:|| :|| :|| :|| :|| :|| :|| :|| :|| :||
 Db 234 FPNWYIISTSQAEHKPVFLGNNSG-QDIDFTMESV 267
 RESULT 14
 JC5646 Interleukin-1 beta - horse
 C;Species: Equus caballus (domestic horse)
 C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 20-Jun-2000
 C;Accession: JC5646
 R;Kato, H.; Youn, H.Y.; Ohashi, T.; Watari, T.; Goitsuka, R.; Tsujimoto, H.; Hasegawa, A;Gene 177, 11-16, 1996
 A;Title: Identification of an alternatively spliced transcript of equine interleukin-1
 A;Reference number: JC5646; MUID:97080493
 A;Accession: JC5646
 A;Molecule type: mRNA
 A;Residues: 1-214 <KAT>
 A;Cross-references: DBSN:Da2165; NID:92463549; PID:BA22528.1; PID:92463550
 C;Comment: This protein mediates a variety of physiological response to infections and i
 synthesis by heptocytes, and stimulation of chondrocytes and synovial cells to produce
 C;Superfamily: interleukin-1

Query Match Best Local Similarity 26.1%; Pred. No. 0.28;
 Best Local Similarity 26.1%; Pred. No. 0.28;
 Matches 35; Conservative 18; Mismatches 50; Indels 31; Gaps 4;
 Matches 35; Conservative 18; Mismatches 39; Indels 1; Gaps 1;
 Qy 69 KDIKLCIFCAETIQGKPTLQKEKNMDLYVERKAQKPFLEFHNEKGSTSVPQSYSPGWFA 128
 Db 145 IRD----MSGPILTAAVINNLEAVKFDMVAVSEEDSQLPVTLRISKTOJFVAQN 197
 C;Accession: A61246; S30572
 R;Andrews, A.E.; Barcham, G.J.; Brandon, M.R.; Nash, A.D.
 Immunology 74, 453-460, 1991
 A;Title: Molecular cloning and characterization of ovine IL-1alpha and IL-1beta.
 A;Reference number: A61246; MUID:92120716
 A;Accession: A61246
 A;Molecule type: mRNA
 R;Fiskerstrand, C.E.; Sargent, D.R.
 A;Residues: 1-268 <AND>
 A;Submitted to the EMBL Data Library, June 1991
 A;Accession: S30572
 A;Molecule type: mRNA
 A;Residues: 1-73, 'V', 75-152, 'M', 154-203, 'H', 205-263, 'L', 265-268 <FTS>
 A;Cross-references: EMBL:X60167; NID:91271; PIR:CA42732.1; PID:91272
 C;Comment: Produced by activated macrophages, the IL-1 proteins stimulate thymocyte prol
 C;Comment: IL-1 proteins are involved in the inflammatory response, being identified as
 C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavage
 C;Superfamily: interleukin-1
 C;Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophag
 F;1-12/Domain: propeptide #status predicted <PRO>
 F;113-2268/Product: interleukin-1 alpha #status predicted <MAT>
 F;82,83/Binding site: myristate (Lys) (covalent) #status predicted

Search completed: May 10, 2002, 09:12:07
 Job time: 107 sec

RESULT 15
 A61245 Interleukin-1 alpha precursor - sheep
 N;Alternate names: hematopoietin-1; IL-1 alpha
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C;Date: 12-May-1994 #sequence_revision 22-Nov-1996 #text_change 28-Jan-2000
 C;Accession: A61245; S30572
 R;Andrews, A.E.; Barcham, G.J.; Brandon, M.R.; Nash, A.D.
 Immunology 74, 453-460, 1991
 A;Title: Molecular cloning and characterization of ovine IL-1alpha and IL-1beta.
 A;Reference number: A61245; MUID:92120716
 A;Accession: A61245
 A;Molecule type: mRNA
 R;Fiskerstrand, C.E.; Sargent, D.R.
 A;Residues: 1-268 <AND>
 A;Submitted to the EMBL Data Library, June 1991
 A;Accession: S30572
 A;Molecule type: mRNA
 A;Residues: 1-73, 'V', 75-152, 'M', 154-203, 'H', 205-263, 'L', 265-268 <FTS>
 A;Cross-references: EMBL:X60167; NID:91271; PIR:CA42732.1; PID:91272
 C;Comment: Produced by activated macrophages, the IL-1 proteins stimulate thymocyte prol
 C;Comment: IL-1 proteins are involved in the inflammatory response, being identified as
 C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavage
 C;Superfamily: interleukin-1
 C;Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophag
 F;1-12/Domain: propeptide #status predicted <PRO>
 F;113-2268/Product: interleukin-1 alpha #status predicted <MAT>
 F;82,83/Binding site: myristate (Lys) (covalent) #status predicted

Query Match 10.8%; Score 88.5; DB 1; Length 268;

Tue May 14 08:26:37 2002

us-09-723-676-2.rpr

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial/
 CC entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC This SWISS-Protein entry is copyright. It is produced through a collaboration -
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial/
 CC entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; M74294; AAA39399.1; -.
 DR EMBL; M64404; AAA39277.1; -.
 DR EMBL; L22838; AAA20576.1; -.
 DR EMBL; M57525; AAA39787.1; -.
 DR EMBL; M63100; AAA39310.1; -.
 DR EMBL; S64082; AAB20265.1; -.
 DR PIR; B40956; B40956.
 DR PIR; A44610; A44610.
 DR HSSP; P18510; ILRA.
 DR MGD; MGI:96547; IL1RN.
 DR InterPro; IPR000975; Interleukin_1.
 DR Pfam; PF00340; IL1; 1.
 DR PRINTS; PRO0264; INTERLEUKIN1.
 DR SMART; SM00125; IL1; 1.
 DR PROSITE; PS00253; INTERLEUKIN_1; 1.
 KW Glycoprotein; Signal.
 FT SIGNAL 1 26 BY SIMILARITY.
 FT CHAIN 27 178 INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN.
 FT DISULFID 92 142 BY SIMILARITY.
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 178 AA; 20274 MW; 84AA002A3119C024 CRC64;
 Query Match 23.9%; Score 195.5; DB 1; Length 178;
 Best Local Similarity 33.6%; Pred. No. 5.5e-12; Matches 49; Indels 25; Gaps 3;
 Matches 49; Conservative 23; Mismatches 49; Indels 25; Gaps 3;
 QY 4 QREAAPKSYAIRDSQQMWMGLNSNLIAAPL-SRSIK-----PTVHLIACRDRDFES 54
 Db 31 KRPCKMKAQFRIWDTNQTKTYLRLNNQLAGYLOGPNPKLKEEKKIDMPVPIDLH----- 80
 QY 55 DKEKGMMWLGKIGKDLCLCEAEIQQKPTIQLEKIMDLYVEKAKQPKLFFHNKEST 114
 Db 81 -----SVFLGIHGKKLCLSAKSQGDKIQLEEVNTIDSANKKEEDKRFTFIRSERKGPT 134
 QY 115 SVFOQSIVSYGFWFMTSTTSCQPIELT 140
 Db 135 TSFESACFGWFCLTLEADHPVSLT 160
 RESULT 2
 ILIX_RAT ID ILIX_RAT STANDARD; PRT; 178 AA.
 AC P25086; DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (IL-1RN)
 GN IL1RN OR IL1RA.
 OS Rattus norvegicus (Rat).
 OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91271363; PubMed=1828896;
 RX PROCESSIONAL NATL ACAD SCI U.S.A. 88:5232-5236(1991).
 RA Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
 RA Brandhuber B.J., Thompson R.C.;
 RT Interleukin 1 receptor antagonist is a member of the interleukin 1
 gene family; evolution of a cytokine control mechanism.;
 RT Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
 CC - FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
 CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
 CC - SIMILARITY: BELONGS TO THE IL-1 FAMILY.

CC
 CC This SWISS-Protein entry is copyright. It is produced through a collaboration -
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial/
 CC entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; M63101; AAC1434.1; -.
 DR PIR; C10956; C40956.
 DR InterPro; IPR000975; Interleukin_1.
 DR Pfam; PF00340; IL1; 1.
 DR PRINTS; PRO0264; INTERLEUKIN1.
 DR SMART; SM00125; IL1; 1.
 DR PROSITE; PS00253; INTERLEUKIN_1; 1.
 DR SIGNAL 1 26 BY SIMILARITY.
 DR CHAIN 27 178 INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN.
 DR DISULFID 92 142 BY SIMILARITY.
 DR CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 178 AA; 20282 MW; F4A5754FB6C5B03 CRC64;
 Query Match 22.4%; Score 183.5; DB 1; Length 178;
 Best Local Similarity 31.9%; Pred. No. 7.9e-11; Matches 45; Indels 15; Gaps 2;
 Matches 45; Conservative 26; Mismatches 55; Indels 15; Gaps 2;
 QY 4 QREAAPKSYAIRDSQQMWMGLNSNLIAAPL-SRSIK-----ADLSRKPVTLIACRDRDFES 59
 Db 31 KRPCKMKAQFRIWDTNQTKTYLRLNNQLAGYLOGPNPKLKEEKKIDMPVPIDLH----- 81
 QY 60 NMVYLGIGKIGKDLCLCFAEIQQKPTIQLEKIMDLYVEKAKQPKLFFHNKEST 119
 Db 82 --VFLGIHGKKLCLSCVKGDDFKLQLEEVNTIDLNKNKEEDKRFTFIRSETGPITSFES 139
 QY 120 VSYPGWETATSTSQGPFLT 140
 Db 140 LACPWFCLTLEADHPVSLT 160
 RESULT 3
 ILIX_HUMAN ID ILIX_HUMAN STANDARD; PRT; 177 AA.
 AC P18510; DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DE INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (ICIL-
 DE IL1RA) (IL-1RN).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90220867; PubMed=2139180;
 RX Carter D.B., Delobel M.R. Jr., Dunn C.J., Tomich C.S.C., Laborde A.L.,
 RA Slichter J.L., Berger A.E., Blenkowski M.J., Sun F.F., McEwan R.N.,
 RA Harris P.K.W., Yem A.W., Waszak G.A., Chosay J.G., Sleu L.C.,
 RA Hardee M.M., Zurich Neely H.A., Reardon I.M., Heinrikson R.L.,
 RA Truesell S.E., Shelly J.A., Fessal T.E., Taylor B.M., Tracey D.E.,
 RT "Purification, cloning, expression and biological characterization of
 RT an interleukin-1 receptor antagonist protein.";
 RN Nature 344:633-638(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90136921; PubMed=2137201;
 RA Eisenberg S.P., Evans R.J., Arend W.P., Verderber E., Brewer M.T.,
 RA Hannun C.H., Thompson R.C.,

- RT "primary structure and functional expression from complementary DNA
of a human interleukin-1 receptor antagonist.";
RL Nature 343:341-346(1990).
RN [3]
- RP SEQUENCE FROM N.A.
- RX MEDLINE=912136; PubMed=1828896;
- RA Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
RA Brandhuber B.J., Thompson R.C.;
RT "interleukin 1 receptor antagonist is a member of the interleukin 1
gene family: evolution of a cytokine control mechanism.";
RT Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
- RL RN [4]
- RP SEQUENCE FROM N.A.
RX MEDLINE=9238323; PubMed=1385987;
- RA Leonard A., Gorman P., Carrier M., Griffiths S., Scootney H.,
RA Sheer D., Solaro R.,
RT "cloning and chromosome mapping of the human interleukin 1
antagonist gene.";
RL Cytokine 4:83-89(1992).
RN [5]
- RP SEQUENCE FROM N.A.
- RX MEDLINE=9714044; PubMed=8992991;
- RA Jenkins J.K., Drong R.F., Shuck M.E., Bienkowski M.J., Slichtom J.L.,
RA Arend W.P., Smith M.F. Jr.,
RT "intracellular IL-1 receptor antagonist promoter: cell type-specific
and inducible regulatory regions.";
RL J. Immunol. 158:748-755(1997).
RN [6]
- RP SEQUENCE OF 26-45.
- RX MEDLINE=90136920; PubMed=2137200;
- RA Hamm C.H., Wilcox C.J., Arend W.P., Joslin F.G., Driops D.J.,
RA Heimdal P.L., Armes L.G., Sommer A., Eisenberg S.P., Thompson R.C.;
RT "Interleukin-1 receptor antagonist activity of a human interleukin-1
inhibitor.";
RL Nature 343:336-340(1990).
RN [7]
- RP SEQUENCE OF 26-52.
- RX MEDLINE=9054444; PubMed=2143761;
- RA Bienkowski M.J., Bessalu T.E., Berger A.E., Truesdell S.E.,
RA Heinrikson R.L., Laborde A.L., Zurich-Neely H.A., Reardon I.M.,
RA "purification and characterization of interleukin 1 receptor level
antagonist proteins from THP-1 cells.";
RL J. Biol. Chem. 265:14505-14511(1990).
RN [8]
- RP SEQUENCE FROM N.A. (INTRACELLULAR FORM).
- RX MEDLINE=91219436; PubMed=1827201;
- RA Hashmi S., Martin G., van Le L., Morris J., Peace A., Bigler C.F.,
RA Jaffee G.J., Hammerberg C., Sporn S.A., Arend W.P., Ralph P.,
RT "cDNA cloning of an intracellular form of the human interleukin 1
receptor antagonist associated with epithelium.";
RT proc. Natl. Acad. Sci. U.S.A. 88:3681-3685(1991).
RN [9]
- RP STRUCTURE BY NMR.
- RX MEDLINE=92297633; PubMed=1534997;
- RA Stockman B.J., Scabill T.A., Roy M., Ulrich E.L., Strakalaitis N.A.,
RA Brunner D.P., Yem A.W., Deibel M.R. Jr.,
RT "Secondary structure and topology of interleukin-1 receptor
antagonist protein determined by heteronuclear three-dimensional NMR
spectroscopy.";
RL Biochemistry 31:5237-5244(1992).
RN [10]
- RP STRUCTURE BY NMR.
- RX MEDLINE=943120651; PubMed=8045306;
- RA Stockman B.J., Scabill T.A., Strakalaitis N.A., Brunner D.P.,
RA Yem A.W., Deibel M.R. Jr.,
RT "Solution structure of human interleukin-1 receptor antagonist
protein.";
RL FEBS Lett. 349:79-83(1994).
RN [11]
- RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
- RX MEDLINE=94230368; PubMed=8175703;
- RA Vigers G.P.A., Caffes P., Evans R.J., Thompson R.C., Eisenberg S.P.,
- RA Brandhuber B.J.;
RT "X-ray structure of interleukin-1 receptor antagonist at 2.0-A
resolution.";
RL J. Biol. Chem. 269:12874-12879(1994).
RN [12]
- RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
- RX MEDLINE=95172072; PubMed=7847645;
- RA Schreuder H.A., Rondeau J.M., Tardif C., Soffientini A., Sarubbi E.,
RA Akeson A., Bowlin T.L., Yanofsky S., Barrett R.W.;
RT "refined crystal structure of the interleukin-1 receptor antagonist.
RT presence of a disulfide link and a cis-proline.";
RL Eur. J. Biochem. 227:838-847(1995).
RN [13]
- RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 32-177 IN COMPLEX WITH IL1R.
- RX MEDLINE=97215904; PubMed=9062194;
- RA Schreuder H., Tardif C., Tripp-Kallmeyer S., Soffientini A.,
RA Sarubbi E., Akeson A., Bowlin T., Yanofsky S., Barrett R.W.;
RT "A new cytokine-receptor binding mode revealed by the crystal
structure of the IL-1 receptor with an antagonist.";
RL Nature 386:194-200(1997).
- CC -1 ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE
SPLICING.
- CC -1 TISSUE SPECIFICITY: THE INTRACELLULAR FORM OF IL-1RA IS
RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
- CC -1 SUBCELLULAR LOCATION: SECRETED OR INTRACELLULAR (THE VARIANT
FORM).
- CC -1 SIMILARITY: BELONGS TO THE IL-1 FAMILY.
- CC -1 DATABASE: NAME=R&D Systems' cytokine source book;
WWW="http://www.rndsystems.com/cyt.cat/il1ra.html".
- CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial/
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
- CC -----
- DR EMBL: MS5646; AAA50138; 1; --.
- DR EMBL: M63099; AAB41943; 1; --.
- DR EMBL: X53296; CA07386; 1; --.
- DR EMBL: X64532; CA4582; 1; --.
- DR EMBL: U65590; AAB92268; 1; --.
- DR EMBL: U65590; AAB92270; 1; --.
- DR PIR: A30368; A30368.
- DR PIR: A37822; A37822.
- DR PIR: S08160; S08160.
- DR PIR: S08159; S08159.
- DR PIR: A40356; A40356.
- DR PIR: A39386; A39386.
- DR PDB: 1ITN; 30-APR-94.
- DR PDB: 2IRY; 15-OCT-94.
- DR PDB: 1IRP; 27-FEB-95.
- DR PDB: 1TR; 07-FEB-95.
- DR PDB: 1IIT; 01-APR-95.
- DR PDB: 1JUN; 17-JUN-98.
- DR Aarhus/Ghent-2DPAGE; 7104; IEF.
- DR Aarhus/Ghent-2DPAGE; 7105; IEF.
- DR MM; 147679; --.
- DR InterPro; IPR000975; Interleukin_1.
- DR Pfam; PF00340; I11; 1.
- DR PR0264; INTERLEUKIN1.
- DR SMART; SM00125; I11; 1.
- DR PROSITE; PS0023; INTERLEUKIN_1; 1.
- FT KW Glycoprotein; Signal; Alternative splicing; 3D-structure.
- FT SIGNAL 1 25
- FT CHAIN 26 177
- FT INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN.
- FT DISULFID 91 141
- FT CARBOHYD 109 109
- N-LINKED (GLCNAC . .) (POTENTIAL).

FT	VARSPLIC	1	21	MELICRGERSHLITLILFFHS -> MAL (IN INTRACELLULAR ISOFORM)	FT	DISULFID	91	141	PROTEIN.			
FT	SEQUENCE	177 AA;	20055 MW;	DB1690776A7394057 CRC64;	FT	CARBOHYD	109	109	BY SIMILARITY.			
Query Match												
QY	4	OREAAPKSYAIRDSRQMVNLSGNSLIAPLSR-----SIKPVLHLIACRDRBFS	54	Best Local Similarity 22.1%; Score 182; DB 1; Length 177; Matches 46; Conservative 27; Mismatches 64; Indels 28; Gaps 4;	FT	CONFLICT	19	19	N-LINKED (GLCNAC. . .) (POTENTIAL).			
Db	30	RKSKRMQAFRIWDYVQKFRLRNQVAVGIVQGPVNLEEKIDVPIPEHAL-----	81	FT	CONFICT	19	19	F -> L (IN REF. 2).				
QY	55	DKEKGNNVVLGIGKDKLCLFCAEIOPKTLQKEKKIMDLVKEKKAQPKFLFFHNKEST	114	FT	SEQUENCE	177 AA;	20459 MW;	1ABC377F1F1C880B CRC64;				
Db	82	-----FLGIHGKGKMCILSCVKSDETRIOLEAVNITDLSNRKDKRFAFRSDGPT	133	QY	4	OREAAPKSYAIRDSRQMVNLSGNSLIAPLRSRSIKPVNLHLIACRDRBFS	54	QY	4	OREAAPKSYAIRDSRQMVNLSGNSLIAPLRSRSIKPVNLHLIACRDRBFS	54	
QY	115	SVQSVSVPVGWFIAATTSQGQPIFLK- ERGITNTNFYLDSE	157	Best Local Similarity 22.2%; Score 182; DB 1; Length 177; Matches 46; Conservative 27; Mismatches 64; Indels 28; Gaps 4;	Db	30	KRPCKM0AFRIWDYVQKFRLRNQVAVGIVQGPVNLEEKIDVPIPEHAL-----	81	QY	4	OREAAPKSYAIRDSRQMVNLSGNSLIAPLRSRSIKPVNLHLIACRDRBFS	54
Db	134	TSFESAAACPGWFCLCTAMEADQPVSITNMPDEGVW-VTKFYFOEDE	177	DEINTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (IL-1RN)	QY	59	GNNVVLGIGKDKLCLFCAEIOPKTLQKEKKIMDLVKEKKAQPKFLFFHNKESTSVFQ	114	Db	78	PDALELGHLGKICLQAVKSGDTEQLEAVNITDLSKKEENRFERRNSGQTTSF	137
RESULT												
IL1X_HORSE	4	STANDARD;	PRT;	177 AA.	Db	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153	QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153
ID	IL1X_HORSE	STANDARD;	PRT;	177 AA.	Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173	Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173
AC	O18999;	077445;	[1]		QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153	QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153
DT	15-DEC-1998	(Rel. 37, Last sequence update)			Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173	Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173
DT	15-DEC-1998	(Rel. 37, Last sequence update)			QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153	QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153
DE	INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (IL-1RN)				Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173	Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173
DE	(IRAP)				QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153	QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153
GN	IL1RN OR IL1RA.				Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173	Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173
OS	EQUUS CABALLUS (Horse).				QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153	QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.				Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173	Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173
OX	NCBI_TAXID=996;				QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153	QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153
RN	1				Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173	Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173
RP	SEQUENCE FROM N.A.				QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153	QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153
RX	MEDLINE=97366446; PubMed=9223227;				Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173	Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173
RA	Kato H., Ohashi T., Matsushiro H., Watari T., Goitsuka R.,				QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153	QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153
RA	Tsujiimoto H., Hasegawa A.;				Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173	Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173
RT	"Molecular cloning and functional expression of equine interleukin-1 receptor antagonist."				QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153	QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153
RT	receptor. Immunol. Immunopathol. 56:221-231(1997).				Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173	Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173
RL	[2]				QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153	QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153
RP	SEQUENCE FROM N.A.				Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173	Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173
RX	MEDLINE=98205942; PubMed=9622739;				QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153	QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153
RA	Howard R.D., McIlwraith C.W., Trotter G.W., Nyborg J.K.,				Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173	Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173
RT	*Cloning of equine interleukin-1 receptor antagonist and determination of its full-length cDNA sequence.;				QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153	QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153
RL	Am. J. Vet. Res. 59:712-716(1998).				Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173	Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173
RP	SEQUENCE FROM N.A.				QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153	QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153
RX	MEDLINE=94165101; PubMed=7509813;				Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173	Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173
RA	Cominelli F., Bortolami M., Pizzarro T.T., Monsacchi L., Ferretti M., Brewer M.T., Eisenberg S.P., Ng R.K.,				QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153	QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153
RT	"Rabbit interleukin-1 receptor antagonist. Cloning, expression, functional characterization, and regulation during intestinal inflammation."				Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173	Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173
RT	J. Biol. Chem. 269:6962-6971(1994).				QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153	QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153
RN	[2]				Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173	Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173
RP	SEQUENCE FROM N.A.				QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153	QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153
RA	Hamada H., Mulligan R.C.; the EMBL/GenBank/databases.				Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173	Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173
RL	Submitted (XXX/99/2) to the EMBL/GenBank/databases.				QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153	QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153
RP	SEQUENCE FROM N.A.				Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173	Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173
RX	MEDLINE=93052512; PubMed=1427977;				QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153	QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153
RA	Goto F., Goto K., Miyata T., Ohwara S., Takao T., Mori S., Furukawa S., Maseda T., Iwanaga S., Shimomishi Y., Yoshinaga M.;				Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173	Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173
RT	"Interleukin-1 receptor antagonist in inflammatory exudate cells of rabbits. Production, purification and determination of primary structure."				QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153	QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153
RT	Immunology 77:235-244(1992).				Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173	Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173
QY	-1- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.				QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153	QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153
CC	-1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.				Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173	Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153	QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153
DR	EMBL; D83714; BAM2259; 1; -.				Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173	Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173
DR	EMBL; U92482; AAC39257; 1. -.				QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153	QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153
DR	InterPro; IPR000975; Interleukin_1.				Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173	Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173
DR	SMART; SM00125; IL1; 1.				QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153	QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153
DR	PROSITE; PS00253; INTERLEUKIN_1; 1.				Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173	Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173
FT	Glycoprotein; Signal.				QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153	QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153
FT	CHAIN				Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173	Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173
FT	1	25	BY SIMILARITY.		QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153	QY	119	SVSYPGNFIATSTSQGQPIFLK- KERGITNTNFYLDSE	153
FT	INTERLEUKIN-1 RECEPTOR ANTAGONIST				Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173	Db	138	SACPGWFCLCTAOEADRPVSLNKPKESFMWTKYL	173

DR EMBL; M57526; AAA31374.1; -.
 DR EMBL; D21832; BAA04860.1; -.
 DR PIR; A54377; A54377.
 DR HSSP; PI8510; ILR.
 DR InterPro; IPR000975; Interleukin_1.
 DR PROSITE; PRO0340; ILL; 1.
 DR SMART; SM00125; ILL; 1.
 DR PRINTS; PRO0264; INTERLEUKIN1.
 DR SMART; SM00125; ILL; 1.
 DR PRINTS; PS00253; INTERLEUKIN_1; 1.
 KW Glycoprotein; Signal.
 FT SIGNAL 1 25
 CHAIN 26 177
 FT DISULFID 91 141
 FT CARBOHYD 109 109
 FT SEQUENCE 177 AA; 20093 MW; 2114DC6119A9D5F9 CRC64;
 SQ
 Query Match 21.8%; Score 178.5; DB 1; Length 177;
 Best Local Similarity 31.2%; Pred. No. 2.7e-10;
 Matches 45; Conservative 21; Mismatches 57; Indels 21; Gaps 2;
 QY 4 QREAPAKSVAIRDSDRSQRMVWVLGSNLIA-----APLSRSIKPVYLHLACRDTEFSDK 56
 Db 30 KRCGCRMQAIFIWVQNKTYFLRNNOVLAGYLOGPNKLAERIDVVYL----- 76
 QY 57 EKGNNMVYLGTGKGDLCIFCAEIQGKPTLQIKEKNIMDVYKEKAQPKPFLFHNKEGSTSV 116
 Db 77 -EPQLLFLGIQRGKLSCVKSGDKMKLHLAVNNTDLGNKNEQDKRFTFIRNSOPTT 135
 QY 117 FQSYSPVGNITATSTSGOPFLTK 140
 Db 136 FESASCPGWFCLTALEADQPVSFT 159

RESULT 6

ILIX_PIG
 ID ILIX_PIG STANDARD; PRT; 177 AA.
 AC 029056;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (IL-1RN)
 DE (IRAP).
 DE (IRAP).
 GN ILRN OR IRAPI.
 OS Sus scrofa (Pig).
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CROSSBREED; TISSUE=Lung;
 RA Yin J., Murtaugh M.P.;
 RT "Characterization of IRAP in morphine treated pig.";
 RL Submitted (May 1996) to the EMBL/GenBank/DDBJ databases.
 CC - FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
 CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
 CC - SIMILARITY: BELONGS TO THE IL-1 FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; L38849; AAA99424.1; -.
 DR InterPro; IPR000975; Interleukin_1.
 DR Pfam; PF00340; ILL; 1.
 DR PRINTS; PRO0264; INTERLEUKIN1.
 DR SMART; SM00125; ILL; 1.
 DR PROSITE; PS00253; INTERLEUKIN_1; 1.

KW Glycoprotein; Signal.
 FT SIGNAL 1 25
 CHAIN 26 177
 FT DISULFID 91 141
 FT CARBOHYD 109 109
 FT SEQUENCE 177 AA; 20093 MW; 2114DC6119A9D5F9 CRC64;
 SQ
 Query Match 21.8%; Score 178; DB 1; Length 177;
 Best Local Similarity 29.6%; Pred. No. 2.7e-10;
 Matches 47; Conservative 20; Mismatches 66; Indels 26; Gaps 3;
 QY 4 QREAPAKSVAIRDSDRSQRMVWVLGSNLIA-----APLSRSIKPVYLHLACRDTEFS 54
 Db 30 KRCGCRMQAIFIWVQNKTYFLRNNOVLAGYLOGPNKLAERIDVVYL----- 79
 QY 55 DKEKGNNMVYLGTGKGDLCIFCAEIQGKPTLQIKEKNIMDVYKEKAQPKPFLFHNKEGST 114
 Db 80 -EPQLLFLGIQRGKLSCVKSGDKMKLHLAVNNTDLGNKNEQDKRFTFIRNSOPTT 133
 QY 115 SVFOSVSYPGWFLATSTSGOPFLTK-ERGTTNNNFY 152
 Db 134 TSFSSAACPGWFCLTALEADQPVGILNTKRAVKVTFY 172

RESULT 7

ILIX_BOVIN
 ID ILIX_BOVIN STANDARD; PRT; 174 AA.
 AC 077482;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (IL-1RN)
 DE (IRAP).
 GN ILRN.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 RA Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 RA Yoshiro T., Iwai H.;
 RT "Enzymatic amplification and expression of bovine interleukin-1
 receptor antagonist cDNA";
 RL Vet. Immunol. Immunopathol. 62:197-208(1998).
 CC - FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
 CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
 CC - SIMILARITY: BELONGS TO THE IL-1 FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; AB005148; BAA31854.1; -.
 DR InterPro; IPR000975; Interleukin_1.
 DR Pfam; PF00340; ILL; 1.
 DR PRINTS; PRO0264; INTERLEUKIN1.
 DR SMART; SM00125; ILL; 1.
 DR PROSITE; PS00253; INTERLEUKIN_1; 1.

KW Glycoprotein; Signal.
 FT SIGNAL 1 23
 CHAIN 24 174
 FT DISULFID 89 139
 FT CARBOHYD 107 107
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ	SEQUENCE	174 AA:	19926 MW;	1E567F224FF851F CRC64;
DR	Query Match	2118;	Score 173;	DB 1;
DR	Best Local Similarity	27.9%;	Pred. No.	8e-10;
DR	Matches	46;	Conservative	24;
DR	Mismatches	57;	Indels	38;
DR	Gaps	4;		
DR	PR1; S23010; S23010.			
DR	HSSP; P01584; 41B3.			
DR	InterPro; IPR002348; IL1_HBGF.			
DR	InterPro; IPR000975; Interleukin_1.			
DR	InterPro; IPR003522; Interleukin_1_prop.			
DR	Pram; PR00340; IL1; 1.			
DR	Pram; PR0294; IL1_propep; 1.			
DR	PRINTS; PR0262; IL1HGF.			
DR	PRINTS; PR00264; INTERLEUKIN1.			
DR	SMART; SM00125; IL1; 1.			
DR	PROSITE; PS00253; INTERLEUKIN_1; 1.			
KW	Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.			
PROPEP	1	113		
FT	CHAIN	114	266	INTERLEUKIN-1 BETA.
FT	CONFFLICT	14	14	Y -> C (IN REF. 2).
FT	CONFFLICT	55	55	Q -> K (IN REF. 2).
FT	CONFFLICT	64	64	V -> A (IN REF. 2).
FT	CONFFLICT	145	145	P -> L (IN REF. 2).
SO	SEQUENCE	266 AA:	30717 MW;	BD007BS8224AB78 CRC64;
RESULT	8			
ID	IL1B_SHEEP	STANDARD;	PRT;	266 AA..
AC	P21621;			
DT	01-MAY-1991 (Rel. 18, Created)			
DT	01-MAR-1992 (Rel. 21, Last sequence update)			
DE	INTERLEUKIN-1 BETA PRECURSOR (IL1-BETA).			
OS	Ovis aries (Sheep).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.			
OC	NEBL_TAXID=9940;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92119335; PubMed=1840515;			
RA	Seow H.F., Rothell J.S., David M.J., Wood P.R.;			
RT	"Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA."			
RL	DNA Seq. 1:423-426(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91080326; PubMed=2263490;			
RA	Fiskerstrand C., Sargan D.;			
RT	"Nucleotide sequence of ovine interleukin-1 beta."			
RL	Nucleic Acids Res. 18:7165-7165(1990).			
CC	-I- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES. IL-1 STIMULATES THYMOCYTE PROLIFERATION BY INDUCING IL2 RELEASE, B-CELL MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.			
CC	IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.			
CC	-I- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.			
CC	-I- MISCCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER SECRETORY PROTEINS.			
CC	-I- SIMILARITY: BELONGS TO THE IL-1 FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; X54796; CAA38566; 1; -.			
CC	EMBL; X56972; CAA40293; 1; -.			
DR	PIR; S13092; S13092.			
DR	PIR; S13810; S13810.			
RESULT	9			
ID	IL1B_BOVIN	STANDARD;	PRT;	266 AA.
AC	P09428;			
DT	01-MAR-1989 (Rel. 10, Created)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).			
GN	IL1B.			
OS	Bos taurus (Bovine).			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Bos.			
OC	NCBI_TAXID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89016591; PubMed=3262866;			
RA	Leong S.R., Flags G.M., Lawman M., Gray P.W.;			
RT	"The nucleotide sequence for the cDNA of bovine interleukin-1 beta."			
RL	Nucleic Acids Res. 16:9054-9054(1988).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=8818652; PubMed=3261832;			
RA	Maliszewski C.R., Baker P.E., Schoenborn M.A., Davis B.S., Cosman D., Gillis S., Cerretti D.P.;			
RT	"Cloning, sequence and expression of bovine interleukin 1 alpha and interleukin 1 beta complementary DNAs."			
RT	Mol. Immunol. 25:429-437(1988).			
RL	-I- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES. IL-1 STIMULATES THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.			
CC	IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.			
CC	-I- SUBUNIT: MONOMER.			

CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
AMINO ENDS OF THESE PROTEINS SERVE AS YET UNDEFINED FUNCTION.
CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
OR IS SECRETED BY A MECHANISM DIFFERENT FROM THAT USED FOR OTHER
SECRETORY PROTEINS.

CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

CC EMBL: M35589; AAA20585_1; -.
DR EMBL: X12498; CAA31018_1; -.
DR EMBL: M37211; AAA0584_1; -.
DR PIR: JI0010; ICB010.
DR PIR: S01380; S01380.
DR HSSP: P01584; I1H1B.
DR InterPro: IPR002348;
DR InterPro: IPR000975; Interleukin_1.
DR InterPro: IPR003502; Interleukin_1_prop.
DR Pfam: PF00340; ILL_1.
DR Pfam: PF02394; ILL_Propep; 1.
DR PRINTS: PRO0362; ILLHGF.
DR SMART: SK00125; ILL_1.
DR PROSITE: PS00253; INTERLEUKIN_1.
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT CHAIN 114 266 AA. A > G (IN REF. 2).
FT CONFLICT 252 262 A
SQ SEQUENCE 266 AA: 30774 MW: 9D1EF8F575070586 CRC64;

Query Match 20.1%; Score 164.5; DB 1; Length 266;
Best Local Similarity 30.7%; Pred. No. 8.7e-09;
Matches 47; Conservative 33; Mismatches 52; Indels 21; Gaps 5;

QY 14 IRRSRQWVWLSGNSLIAAPLRSRKPVTHLIA--CRDTEF---SDREKGNNM--VV 63
DB 123 LQDREQKSLVLYASPCVLKA-----LHLLSQEMNREWFVCFMSFVQGERDNKIPVA 172

QY 64 LGIKGKDGLCFCATIQGKPTQLKEKKNMIDYVVKQAQKPLFFHINKEGSPISVFSVSYP 123
DB 173 LGIKDKNLYLSCVKGDTPLQLEED-PKVPKRNMEKREVYKEIKNTVFEFESVLYP 231

QY 124 GWFTATSTSGQPIFLTKERGITNTNFYLDV 156
DB 232 NWYIYSTSQLEERPFLGHFRAGQDITDFRMETL 264

RESULT 10

ID IL1B_HUMAN STANDARD: PRT; 269 AA.

AC P01584;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA) (CATABOLIN).

GN IL1B.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:85088517; PubMed=6083565;
RA Auton R.E., Webb A.C., Rosenvasser L.J., Mucci S.F., Rich A.,
RA Wolff S.M., Binarelli C.A.;
RA Wolff S.M., Dinarrello C.A., Rosenwasser L.J., Mucci S.F., Rich A.,
RA Nishida T., Nishijo N., Takano M., Kawai K., Bando K., Masui Y.,
RA Nakai S., Hirai Y.;
RT "cDNA cloning of the mRNA coding for human prointerleukin-1 alpha and
prointerleukin-1 beta.", Dokl. Akad. Nauk SSSR 309:1005-1008(1989).
RN [6]
RP SEQUENCE FROM N.A.
RA Webb A.C., Dinarrello C.A., Rosenwasser L.J., Mucci S.F., Rich A.,
RT "Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.",
RL Adv. Gene Technol. 22:339-340(1985).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE:87156769; PubMed=3493774;
RA Nishida T., Nishijo N., Takano M., Kawai K., Bando K., Masui Y.,
RA Nakai S., Hirai Y.;
RT "cDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell
line.", Biochem. Biophys. Res. Commun. 143:345-352(1987).
RL Blood. Biophys. Res. Commun. 143:345-352(1987).
RN [8]
RP SEQUENCE OF 117-128.
RX MEDLINE:88184226; PubMed=3281727;
RA Zsebo K.M., Wypych J., Yuschenkooff V.N., Lu H., Hunt P., Dukes P.P.,
RA Langley K.E.;
RT "Effects of hematopoietin-1 and interleukin 1 activities on early
hematopoietic cells of the bone marrow.",
RL Blood 71:962-968(1988).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX MEDLINE:8821154; PubMed=3259176;
RA Priestle J.P., Schor H.-P., Grutter M.G.;
RT "Crystal structure of the cytokine interleukin-1 beta.",
RL EMBO J. 7:339-343(1988).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE:9009325; PubMed=2602367;
RA Priestle J.P., Schor H.-P., Grutter M.G.;
RT "Crystalllographic refinement of interleukin 1 beta at 2.0-A
resolution.",
RL Proc. Natl. Acad. Sci. U.S.A. 86:9667-9671(1989).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE:90064532; PubMed=2585509;
RA Finzel B.C., Clancy L.L., Holland D.R., Muchmore S.W.,

RA Watenpaugh K.D.; Einspahr H.M.;
RT "Crystal structure of recombinant human interleukin-1 beta at 2.0-A
resolution";
RL J. Mol. Biol. 209:779-791(1989).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) IN COMPLEX WITH RECEPTOR.
RX MEDLINE=97215903; PubMed=9062193;
RA Vigers G.P.; Anderson L.J.; Caffes P.; Brandhuber B.J.;
RT "Crystal structure of the type-I interleukin-1 receptor complexed
with interleukin-1beta";
RL Nature 386:190-194(1997).
RN [13]
RP STRUCTURE BY NMR.
RX MEDLINE=90321925; PubMed=2372550;
RA Driscoll P.C.; Gronenborn A.M.; Wingfield P.T.; Clore G.M.;
RT "Determination of the secondary structure and molecular topology of
interleukin-1 beta by use of two- and three-dimensional heteronuclear
15N-1H NMR spectroscopy";
RL Biochemistry 29:4668-4682(1990).
RN [14]
RP STRUCTURE BY NMR.
RX MEDLINE=91159409; PubMed=2001363;
RA Clore G.M.; Wingfield P.T.; Gronenborn A.M.;
RT "High-resolution three-dimensional structure of interleukin 1 beta in
solution by three- and four-dimensional nuclear magnetic resonance
spectroscopy";
RL Biochemistry 30:2315-2323(1991).
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE. B-CELL
MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC ID-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -!- SUBUNIT: MONOMER.
CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
SECRETORY PROTEINS.
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration -
the European Bioinformatics Institute. There are no restrictions on its
use by non profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC EMBL: M15840 AAA74137.1; -
DR EMBL; X02532 CA26372.1; -
DR EMBL; K02770; AAA56106.1; -
DR EMBL; X04500; CA428185.1; -
DR EMBL; X56007; CA39557.1; -
DR EMBL; M54933; AAA59136.1; -
DR EMBL; M15330; AAA59135.1; -
DR PIR; A0184; ICHUB; -
DR PIR; A25542; A25542.
DR PIR; A25019; A25019.
DR PIR; A27615; B27615.
DR PIR; S19626; S19626.
DR PDB; 1IIB; 15-OCT-92.
DR PDB; 2IIB; 15-APR-92.
DR PDB; 3IIB; 15-APR-92.
DR PDB; 4IIB; 15-JUL-92.
DR PDB; 5IIB; 15-OCT-94.
DR PDB; 6IIB; 15-OCT-92.
DR PDB; 7IIB; 15-OCT-92.
DR PDB; 21BI; 15-APR-92.
DR PDB; 31BI; 15-APR-92.
DR PDB; 41BI; 15-JUL-92.
DR PDB; 1HIB; 31-JAN-94.
DR PDB; 1I0B; 17-AUG-96.

RESULT	11
IL1B_FELCA	
IL1B_FELCA	STANDARD;
ID	PRT;
AC	267 AA.
DT	01-NOV-1995 (Rel. 32, Created)
DT	01-NOV-1995 (Rel. 32, Last sequence update)
DT	30-MAY-2000 (Rel. 39, Last annotation update)
DE	INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
GN	IL1B.
OS	Felis silvestris catus (Cat).
OC	Bukarota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX	NCBI_TaxID=9685;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Bone marrow;
RA	Daniel S.L., Brenner C.A., Legende A.M., Solomon A., Rouse B.T.,

RL Submitted (XXX-1993) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
 CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
 CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
 CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
 CC -!- SUBUNIT: MONOMER.
 CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
 CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
 CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
 CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
 CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
 CC SECRETORY PROTEINS.
 CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; M2060; AAA0814.1; -.
 DR HSSP; P01584; IHTB.
 DR InterPro; IPR002348; IL1_HBGF.
 DR InterPro; IPR000975; Interleukin_1.
 DR InterPro; IPR003502; Interleukin_1_prop.
 DR Pfam; PF00340; ILL_1.
 DR Pfam; PF02394; ILL_Propep; 1.
 DR PRIMIS; PR00262; IL1HBGF.
 DR PRIMIS; PR0264; INTERLEUKIN1.
 DR SMART; SM00125; ILL_1.
 DR PSITE; PS00253; INTERLEUKIN_1; 1.
 KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
 FT PROPEP 115 BY SIMILARITY.
 FT CHAIN 116 267 AA; 30361 MW; 781F9971E32F6A61 CRC64;
 SQ SEQUENCE 267 AA; 30361 MW; 781F9971E32F6A61 CRC64;
 RESULT 12
 IL1B_CEREL
 ID IL1B_CEREL STANDARD; PRT; 266 AA.
 AC P51745;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
 IL1B
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
 OC Cervidae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Lockhart E.A.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
 CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
 CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
 CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
 CC -!- SUBUNIT: MONOMER.
 CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
 CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
 CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
 CC SECRETORY PROTEINS.
 CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; U20500; AAA62234.1; -.
 DR HSSP; P01584; IHTB.
 DR InterPro; IPR002348; IL1_HBGF.
 DR InterPro; IPR000975; Interleukin_1.
 DR InterPro; IPR003502; Interleukin_1_prop.
 DR InterPro; IPR003502; Interleukin_1.
 DR Pfam; PF00340; ILL_1.
 DR Pfam; PF02394; ILL_Propep; 1.
 DR PRIMIS; PR00262; IL1HBGF.
 DR PRIMIS; PR00264; INTERLEUKIN1.
 DR SMART; SM00125; ILL_1.
 DR PROSITE; PS00253; INTERLEUKIN_1; 1.
 KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
 FT PROPEP 113 BY SIMILARITY.
 FT CHAIN 114 266 AA; 30629 MW; 4F40B4E6F0D9F060 CRC64;
 SQ SEQUENCE 266 AA; 30629 MW; 4F40B4E6F0D9F060 CRC64;
 RESULT 13
 IL1B_PIG
 ID IL1B_PIG STANDARD; PRT; 267 AA.
 AC P26889;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
 IL1B
 OS Sus scrofa (Pig).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;

Tue May 14 08:26:37 2002

us-09-723-676-2.rsp

Page 12

OM protein - protein search, using sw model

copyright (c) 1993 - 2000 Compugen Ltd.

Run on: May 10, 2002, 09:10:45 ; Search time 24.55 Seconds
(without alignments)
935.428 Million cell updates/sec

title: US-09-723-676-2

Perfect score: 818

Sequence: 1 MNPOREAAPKSYAIRDSRQM..... FLTKERGITTNNFYLDLDSVE 157

Scoring table: BLOSUM62

gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPREMBBL17:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_plage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	818	100.0	157	4	Q9HAA5	Q9hah5 homo sapien
2	516	103.1	11	09D626	09d626 mus musculus	
3	452	55.3	164	4	Q9NZH7	Q9nz7 homo sapien
4	385	47.1	158	4	Q9HAA7	Q9nah7 homo sapien
5	345.5	42.9	169	4	Q9VHZ8	Q9vhz8 homo sapien
6	293.5	35.9	160	11	Q9JLA2	Q9jla2 mus musculus
7	229	28.0	192	4	Q9HAB6	Q9hab6 homo sapien
8	229	28.0	218	4	Q9HBF3	Q9hbf3 homo sapien
9	229	28.0	218	4	Q9BHO0	Q9bho0 homo sapien
10	200.5	24.5	155	4	Q9YQY1	Q9yy1 mus musculus
11	198.5	24.3	155	11	Q9JIG2	Q9jig2 mus musculus
12	198.5	24.3	156	11	Q9JLA2	Q9jla2 mus musculus
13	195.9	23.9	159	11	Q9D207	Q9d207 mus musculus
14	182.5	22.3	178	4	Q9HBF2	Q9hbf2 homo sapien
15	182	22.2	180	4	Q1628	Q14628 homo sapien
16	181	22.1	143	4	Q9UPCO	Q9upco homo sapien
17	176.5	21.6	6	09BHO	Q9bho canis familiaris	
18	176	21.5	144	4	Q9BYX1	Q9byx1 homo sapien
19	177	6	99GM24	99gm24 tursiops tr		

ALIGNMENTS

RESULT 1

RESULT	1
Q9UHA5	PRELIMINARY;
Q9UHA5	PRT; 157 AA.
AC	
DT	01-MAY-2000 (TREMBBL1. 13, created)
DT	01-MAY-2000 (TREMBBL1. 13, last sequence update)
DT	01-JUN-2001 (TREMBBL1. 17, Last annotation update)
DE	FILL ERA.
OS	Homo sapiens (Human)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=2009288; PubMed=10625660;
RA	Smith D.E., Renshaw B.R., Ketcham R.R., Rubin M., Garka K.E., RA
RA	Sims J.E., J. Biol. Chem. 275:1169-1175(2000).
RT	"Four New Members Expand the IL-1 Superfamily.";
RT	EMBL; AF20183; AAF25213.1; -
DR	HSSP; P10749; 2NIB.
DR	InterPro; IPR000975; Interleukin_1.
DR	Pfam; PF00340; ILI; 1.
DR	SMART; SW00125; ILI; 1.
DR	PROSITE; PS00023; INTERLEUKIN_1; UNKNOWN_1.
SQ	SEQUENCE 157 AA; 17702 MW; 7A5413D7557A3E3 CRC64;

Query Match 100.0%; score 818; DB 4; Length 157; Best Local Similarity 100.0%; Pred. 3.3e-76; Indels 0; Gaps 0; Matches 157; Conservative 0; Mishatches 1.

QY 1 MNPOREAAPKSYAIRDSRQM.....FLTKERGITTNNFYLDLDSVE 157

Db 1 MNPOREAAPKSYAIRDSRQM.....FLTKERGITTNNFYLDLDSVE 157

QY 61 MYLGIGRKDKTCILFCABIOGKPLQLKEKNMDLYVERKAQPKPLFFHNGESTSVRSV 120

Db 61 MYLGIGRKDKTCILFCABIOGKPLQLKEKNMDLYVERKAQPKPLFFHNGESTSVRSV 120

QY 121 SYPGWATATSTSGQPFLTKEGITTNNFYLDLDSVE 157

OY	129	TSTSGQPIFLTKERGTTNTNFYL	153	OX	NCBL_TAXID=10090;			
ID	Q9NZH8	PRELIMINARY;	PRT;	RN	[1]			
AC	Q9NZH8;			RP	SEQUENCE FROM N.A.			
DT	01-OCT-2000	(TREMBLrel. 15, Created)		RX	MEDLINE=20209405; PubMed=10744718;			
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)		RA	Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N., Doyle M.L., Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Young P.R.,			
DE	INTERLEUKIN-1 HOMOLOG 1 (INTERLEUKIN-1 EPSILON).			RA	"Identification and initial characterization of four novel members of the interleukin-1 family";			
GN	IL1E			RL	J. Biol. Chem. 275:10308-10314(2000).			
OS	Homo sapiens (Human).			RN	[2]			
OC	Mammalia; Eutheria; Primates; Catarrhini; Vertebrata; Euteleostomi; OX			RA	Debets R., Timans J., Zurawski S., Bazan J.-F., Kastlein R.A.; "Novel IL-1 family member IL-1e responds through the orphan IL-1R-related protein 2; response is antagonized by IL-1d.";			
	NCBI-TaxID=9606;			RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.			
RN	[1]			RN	[3]			
RP	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.			
RX	MEDLINE=20209405; PubMed=10744718;			RC	SEQUENCE FROM N.A.			
RA	Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N., Doyle M.L., Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Young P.R.,			RC	STRAIN=C57BL/6J; TISSUE=EMBRYO;			
RA	Young P.R., Timans J., Zurawski S., Bazan J.-F., Kastlein R.A.; "Identification and initial characterization of four novel members of the interleukin-1 family";			RC	MEDLINE=21085660; Pubmed=11217851;			
RT	"Identification and initial characterization of four novel members of the interleukin-1 family";			RX	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Iizuka K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakada S., Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R., Kadori K., Matsuda H.A., Ashburner M., Batalov S., Casarant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nakatado I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Borrelli D., Boujunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M., Gustincich S., Hill D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P., Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N., Sasaki H., Sato K., Schoebach C., Seva T., Shibaoka Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kontsuki S., Hayasizaki Y.,		RA	Gustincich S., Hill D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P., Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N., Sasaki H., Sato K., Schoebach C., Seva T., Shibaoka Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kontsuki S., Hayasizaki Y.,
RT	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.			RA	"Functional annotation of a full-length mouse cDNA collection.";			
RL	EMBL: AF20492; AAF6248.1; -.			RA	Nature 409:685-690(2001);			
DR	InterPro; IPR00975; Interleukin_1.			RA	EMBL: AF20493; AAF6249.1; -.			
DR	SMART; SM00125; ILL; 1.			RA	EMBL: AF206697; AAG35671.1; -.			
DR	SEQUENCE 169 AA; 18721 MW; F00A9243706F4154 CRC64;			DR	MGB; MGI:1859324; Fill;			
DR	Best Local Similarity 45.0%; Pred. No. 9; 8e-28; Matches 68; Conservative 29; Mismatches 53; Indels 1; Gaps 1;			DR	InterPro; IPR00975; Interleukin_1.			
OY	4	OREAAPKSYAIRDSRSQAVWLSGNSLIAPLSRSIKPVTIHLTACRDTEFSDEKKGNMVT	63	DR	Nature 409:685-690(2001);			
Db	17	OSMKPKITGTGINDLNQQWTLQGQNLTAVPRSVDSTPVTIVAVTCKYPALEGRGDPTY	76	DR	EMBL: AF206697; AAG35671.1; -.			
Db	64	LIGIKGDICLFCAEIQSKPTLQKEKNMDLYVEKACKPFLPFPHNKRGSTSVSQVSVP	123	DR	MGB; MGI:1859324; Fill;			
Db	77	LGIONPENCPCLYCEKVGQSOPTLQIKEQKMDLGQPEPKFLYRAKIGRTSISLESVAPP	136	DR	InterPro; IPR00975; Interleukin_1.			
OY	124	GWFIAATSTSGQPIFLTKERGTTNTNFYL	154	DR	SMART; SM00125; ILL; 1.			
Db	137	DWEIASKRKD-QPILITSELGSKSYNTAFLN	166	DR	SEQUENCE 160 AA; 18015 MW; AA0434D68FF62F4A CRC64;			
RESULT	6			DR				
Q9JLA2				DR				
ID	Q9JLA2	PRELIMINARY;	PRT;	RN	Query Match 35.9%; Score 293.5; DB 11; Length 160;			
AC	Q9JLA2;			RP	Best Local Similarity 37.7%; Pred. No. 2e-22; Matches 58; Conservative 31; Mismatches 62; Indels 3; Gaps 1;			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			RA	MAPORE--ARKSYAIRDSRSQAVWLSGNSLIAPLSRSIKPVTIHLTACRDTEFSKE 57			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			DB	1 MKKEKELRAASLSLRVQDLSRSLNNLITAVPRREQTVPVITLPCQVQDITLEN 60			
DE	INTERLEUKIN-1 HOMOLOG 1 (INTERLEUKIN-1 EPSILON) (INTERLEUKIN 1			QY	KSNMVYLGIGKGDICLFCAEIQSKPTLQKEKNMDLYVEKACKPFLPFPHNKRGSTSVF 117			
DE	INTERLEUKIN-1 HOMOLOG 1 (INTERLEUKIN-1 EPSILON) (INTERLEUKIN 1			DB	61 RDGPTYMGVORPMSCLFCITDGFQPVQVLGEQNMEMINKMENKPVKASLYHKSGTSIF 120			
DE	FILL OR TLL.			QY	OSVSYGPMFIATSTSGQPIFLTKERGTTNTNFYL			
OS	SUPERFAMILY 1, EPSILON).			ID	Q9UHA6			
OS	MUS musculus (Mouse).			AC	Q9UHA6;			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; MUS.			DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			

DT 01-JUN-2001 (TREMBrel. 17, Last annotation update)
DE FILL ZETA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Buttheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TAXID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092888; PubMed=10625650;
RA Smith D.E.; Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
RA Sims J.E.;
RT "Four New Members Expand the IL-1 Superfamily";
RL J. BIOL. CHEM. 275:1169-1175(2000).
DR EMBL: AF201832; AAF25212.1; -.
DR HSSP: P18510; IITN.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IIL; 1.
DR SMART: SM00125; ILL; 1.
SQ SEQUENCE 192 AA; 21543 MW; 4AF584C81802F612 CRC64;

Query Match 28.0%; Score 229; DB 4; Length 192;
Best Local Similarity 34.8%; Pred. No. 1.e-15; Indels 4; Gaps 3;
Matches 47; Conservative 33; Mismatches 51; Index 4; Gaps 3;

QY 9 PKSYAIRDQRQWVLSGNSLIAAPLSRSIKPVTLHLIACRDTESDKEKGNNVYLGIKG 68
Db 31 PPKFSIHQDKHVQLVLDSGNLIAVPDKNYIRPEFFALAA-SSLSASAEGSPILLGVSK 89

QY 69 KDLCLFCAEIQGK--PTLQLEKKNIMLYVEKK-AQKPFLEFFHNKEGSTSVFQSVSYPGW 125
Db 90 GEFCLYCDKQGSHSLSQKKERKLMLAAQKESARRPFPFYRAQVGSWNMLESAAHPGW 149

QY 126 FIATSTTSQGPILFT 140
Db 150 FICTSNCNCNEPVGVT 164

RESULT 8

Q9NZH6 PRELIMINARY; PRT; 218 AA.
ID Q9NZH6
AC 09NZH6
DT 01-OCT-2000 (TREMBrel. 15, Created)
DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBrel. 17, Last annotation update)
DE INTERLEUKIN-1 HOMOLOG 4 (IL-1X PROTEIN) (INTERLEUKIN-1-RELATED PROTEIN
DE LONG ISOFORM A).
OS Homo sapiens (Human).
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA Pan G.; Risser P.; Mao W.; Baldwin D.T.; Zhong A.W.; Yansura D.,
RA Lewis L.; Eigenbrot C.; Henzle W.J.; Vandlen R.; Filvaroff E.,
RT "IL-1H", an interleukin-1-related protein that binds IL-18 receptor/IL-1
RT Submitted (APR-2000) to the EMBL/GenBank/DDJB databases.
DR EMBL: AF251119; AAC14421.1; -.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; ILL; 1.
DR SMART: SM00125; ILL; 1.
SQ SEQUENCE 218 AA; 24138 MW; 76B09C35093DEA63 CRC64;

Query Match 28.0%; Score 229; DB 4; Length 218;
Best Local Similarity 34.8%; Pred. No. 1.2e-15; Indels 4; Gaps 3;
Matches 47; Conservative 33; Mismatches 51; Index 4; Gaps 3;

QY 9 PKSYAIRDQRQWVLSGNSLIAAPLSRSIKPVTLHLIACRDTESDKEKGNNVYLGIKG 68
Db 57 PPKFSIHQDKHVQLVLDSGNLIAVPDKNYIRPEFFALAA-SSLSASAEGSPILLGVSK 115

QY 69 KDLCLFCAEIQGK--PTLQLEKKNIMLYVEKK-AQKPFLEFFHNKEGSTSVFQSVSYPGW 125
Db 116 GEFCLYCDKQGSHSLSQKKERKLMLAAQKESARRPFPFYRAQVGSWNMLESAAHPGW 175

QY 126 FIATSTTSQGPILFT 140
Db 176 FICTSNCNCNEPVGVT 190

RESULT 9

Q9HBF3 PRELIMINARY; PRT; 218 AA.
ID Q9HBF3
AC 09HBF3;
DT 01-MAR-2001 (TREMBrel. 16, Created)
DT 01-MAR-2001 (TREMBrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBrel. 17, Last annotation update)
DE INTERLEUKIN-1-RELATED PROTEIN LONG ISOFORM.
OS Homo sapiens (Human).
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA Pan G.; Risser P.; Mao W.; Baldwin D.T.; Zhong A.W.; Yansura D.,
RA Lewis L.; Eigenbrot C.; Henzle W.J.; Vandlen R.; Filvaroff E.,
RT "IL-1H", an interleukin-1-related protein that binds IL-18 receptor/IL-1
RT Submitted (APR-2000) to the EMBL/GenBank/DDJB databases.
DR EMBL: AF251119; AAC14421.1; -.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; ILL; 1.
DR SMART: SM00125; ILL; 1.
SQ SEQUENCE 218 AA; 24138 MW; 76B09C35093DEA63 CRC64;

Query Match 28.0%; Score 229; DB 4; Length 218;
Best Local Similarity 34.8%; Pred. No. 1.2e-15; Indels 4; Gaps 3;
Matches 47; Conservative 33; Mismatches 51; Index 4; Gaps 3;

QY 9 PKSYAIRDQRQWVLSGNSLIAAPLSRSIKPVTLHLIACRDTESDKEKGNNVYLGIKG 68
Db 57 PPKFSIHQDKHVQLVLDSGNLIAVPDKNYIRPEFFALAA-SSLSASAEGSPILLGVSK 115

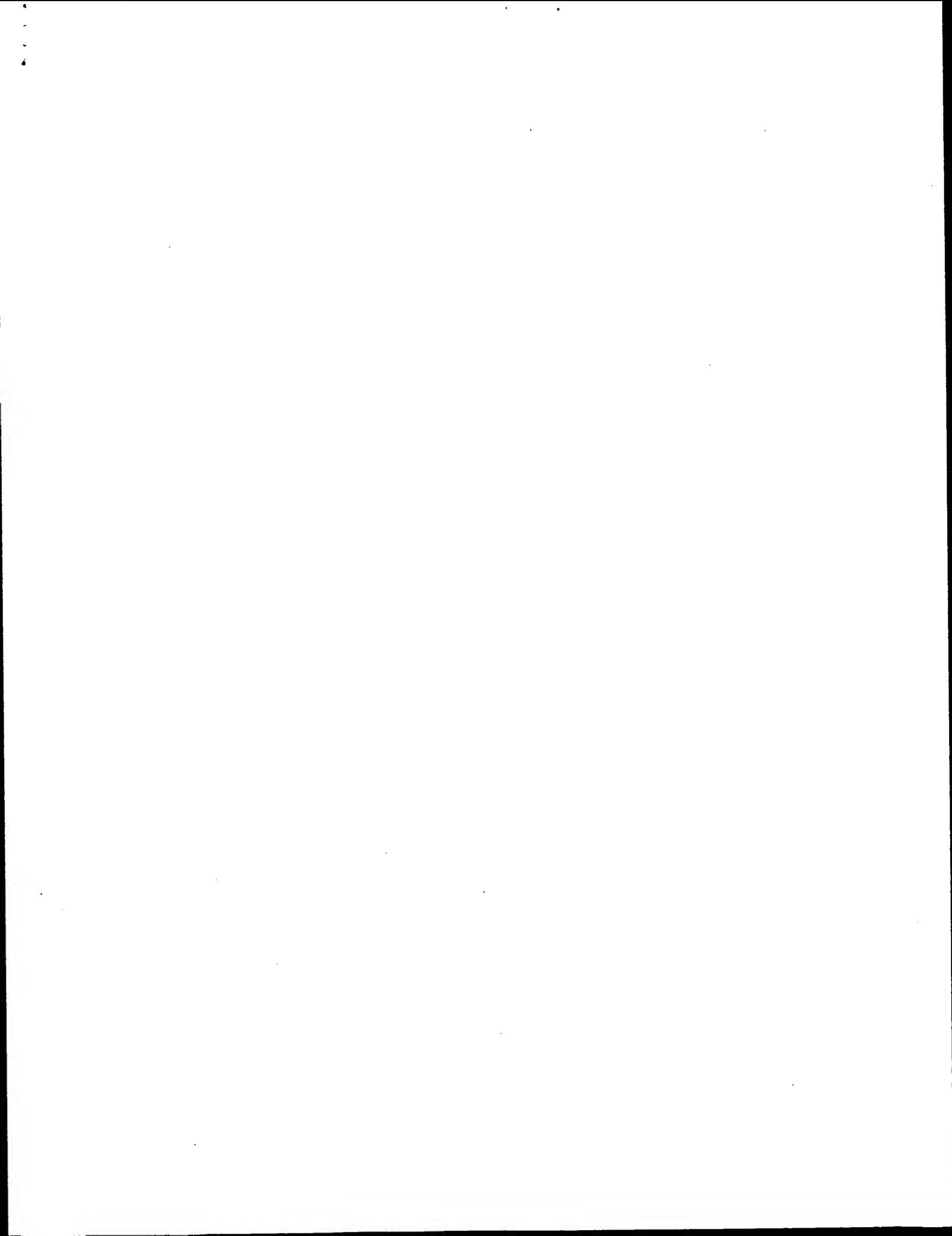
QY 69 KDLCLFCAEIQGK--PTLQLEKKNIMLYVEKK-AQKPFLEFFHNKEGSTSVFQSVSYPGW 125
Db 116 GEFCLYCDKQGSHSLSQKKERKLMLAAQKESARRPFPFYRAQVGSWNMLESAAHPGW 175

QY 126 FIATSTTSQGPILFT 140
Db 176 FICTSNCNCNEPVGVT 190

RESULT 10

ID Q9UBH0 PRELIMINARY; PRT; 155 AA.

AC	Q9BQH0;
DT	01-MAY-2000 (TREMBrel. 13, Last sequence update)
DT	01-MAY-2000 (TREMBrel. 13, Last annotation update)
DT	01-JUN-2001 (TREMBrel. 17, Last annotation update)
DE	F11 DELTA (INTERLEUKIN-1 LIKE PROTEIN 1) (INTERLEUKIN-1 RECEPTOR ANTAGONIST HOMOLOG 1) (INTERLEUKIN-1 DELTA).
GN	IL1HY1 OR IL1L.
OC	Homo sapiens (Human).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC	NCBI_TaxID=9606;
RN	[1] NCBI_TaxID=9606;
RP	SEQUENCE FROM N.A.
RX	MEDLINE=20092888; PubMed=10625660;
RA	Smith D.E., Renshaw B.R., Ketcham R.R., Kubin M., Garka K.E., Sims J.E.;
RA	"Four New Members Expand the IL-1 Superfamily.";
RT	J. Biol. Chem. 275:1169-1175(2000).
RN	[2] SEQUENCE FROM N.A.
RP	MEDLINE=9943727; PubMed=10512743;
RA	Mulero J.J., Pace A.M., Neikin S.T., Loeb D.B., Correa T.R., Drmanac R., Ford J.E.;
RA	"IL1HY1: A Novel Interleukin-1 Receptor Antagonist Gene.";
RT	Biochem. Biophys. Res. Commun. 263:702-706(1999).
RN	[3] SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
RC	TISSUE=PLACENTA;
RA	Barton J.L., di Giovine F.S., Symons J.A., Nicklin M.J.H.; "A tissue specific interleukin-1 receptor antagonist homolog from the IL1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18ra activities.";
RT	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN	[4] SEQUENCE FROM N.A.
RA	Barton J.L., Herbst R., Bosisio D., Nicklin M.J.H.;
RT	"A tissue specific interleukin-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18ra activities.";
RT	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN	[5] SEQUENCE FROM N.A.
RP	MEDLINE=2032477; PubMed=10866108;
RA	Mulero J.J., Nelken S.T., Ford J.E.;
RA	"Organization of the Human Interleukin-1 Receptor Antagonist Gene [6] Immunogenetics 51:425-428(2000).
RN	SEQUENCE FROM N.A.
RA	Debets R., Timans J.C., Zurawski S., Sana T.R., Bazan F., Kastlein R.A., "Novel IL-1 ligands IL-1 α and IL-1 β use IL-1R related protein 2.";
RT	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RL	Best Local Similarity 36.6%; Pred. No. 1e-12; Length 155; Matches 49; Conservative 22; Mismatches 52; Indels 11; Gaps 4; Gaps
DR	EMBL; AF201800; AF252101; -;
DR	EMBL; AF186044; AF027571; -;
DR	EMBL; AF242777; CAB59822; -;
DR	EMBL; AT242738; CAB59823; -;
DR	EMBL; AU271396; CAB67705; -;
DR	EMBL; AF216693; AAF76981; -;
DR	EMBL; AF230377; AAQ91274; -;
DR	HSSP; P18510; IL1R.
DR	InterPro; IPR000975; Interleukin_1.
DR	PFAM; PF00340; IL1; 1.
DR	SMART; SM00125; IL1; 1.
DR	PROSITE; PS00253; INTERLEUKINT_1; 1.
SQ	SEQUENCE 155 AA; 17004 MW; A4B1770F2E12533A CRC64;
Query Match	24.5%; Score 200.5; DB 4; Length 155;
Best Local Similarity	35.1%; Pred. No. 6.5e-13; Indels 15; Gaps 6;
Matches	54; Conservative 24; Mismatches 61; Indels 15; Gaps 6;
QY	12 YARD5R0WVWVLSGNSLIAPL--SRSTKPVTLHLACR--DTEFSDEKEGNMVIGIK 67
QY	12 YARD5R0WVWVLSGNSLIAPL--SRSTKPVTLHLACR--DTEFSDEKEGNMVIGIK 67
Db	9 FRMKDSALKVLYKHNLQLLAGLHLRKEVKGEEISWPVNRAIDLASLSP-----VILGQ 62
QY	68 GKICLGFCAEIQSKPTOLKEKNTMDLYVEKKKAQPLFFHNKEGSTSFTFRRDGMGTSSFESSRAYPOWF 127
Db	63 GGSQCLSGCTEGK-PILKIEPVNIMELYIGAKESISFTFRRDGMGTSSFESSRAYPOWF 121
QY	128 ATSTTSQGPILFK 141
Db	122 CTSPEADQPVRLTQ 135
RESULT	11
ID	Q9QYV1
PRELIMINARY;	PRT; 155 AA.
AC	Q9QYV1;
DT	01-MAY-2000 (TREMBrel. 13, Last sequence update)
DT	01-MAY-2000 (TREMBrel. 13, Last annotation update)
DT	01-JUN-2001 (TREMBrel. 17, Last annotation update)
DE	IL1HY1 PROTEIN (INTERLEUKIN-1 HOMOLOG 3).
GN	IL1HY1.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1] SEQUENCE FROM N.A.
RP	"IL-1IL1: A Novel Member of the Interleukin-1 Gene Family is Expressed in Trophoblasts and Macrophages.";
RT	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN	[2] SEQUENCE FROM N.A.
RP	"IL-1IL1: Nicklin M.J.H.; Barton J.L., Nicklin M.J.H.; Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RL	Best Local Similarity 36.6%; Pred. No. 1e-12; Length 155; Matches 49; Conservative 22; Mismatches 52; Indels 11; Gaps 4; Gaps
DR	EMBL; AJ250429; CAB59831; 1; -;
DR	EMBL; AF200495; AA69251; 1; -;
DR	HSSP; P18510; IL1R.
DR	MGD; MGD:1859325; IL1HY1.
DR	InterPro; IPR000975; Interleukin_1.
DR	PFAM; PF00340; IL1; 1.
DR	SMART; SM00125; IL1; 1.
DR	PROSITE; PS00253; INTERLEUKINT_1; 1.
SQ	SEQUENCE 155 AA; 17004 MW; A4B1770F2E12533A CRC64;
Query Match	24.3%; Score 198.5; DB 11; Length 155;
Best Local Similarity	36.6%; Pred. No. 1e-12; Length 155;
Matches	49; Conservative 22; Mismatches 52; Indels 11; Gaps 4; Gaps
QY	12 YARD5R0WVWVLSGNSLIAPL--SRSTKPVTLHLACR--DTEFSDEKEGNMVIGIK 67
Db	9 FRMKDSALKVLYKHNLQLLAGLHLRKEVKGEEISWPVNRAIDLASLSP-----VILGQ 62
QY	68 GKICLGFCAEIQSKPTOLKEKNTMDLYVEKKKAQPLFFHNKEGSTSFTFRRDGMGTSSFESSRAYPOWF 127
Db	63 GGSQCLSGCTEGK-PILKIEPVNIMELYIGAKESISFTFRRDGMGTSSFESSRAYPOWF 121
QY	128 ATSTTSQGPILFK 141
Db	122 CTSPEADQPVRLTQ 135
RESULT	12
ID	Q9JIG2
PRELIMINARY;	PRT; 156 AA.
AC	Q9JIG2;
DT	01-OCT-2000 (TREMBrel. 15, Last sequence update)
DT	01-OCT-2000 (TREMBrel. 15, Last annotation update)
DE	FRNKDSALKVLYKHNLQLLAGLHLRKEVKGEEISWPVNRAIDLASLSP-----VILGQ 62
GN	GGSQCLSGCTEGK-PILKIEPVNIMELYIGAKESISFTFRRDGMGTSSFESSRAYPOWF 121
QY	68 GKICLGFCAEIQSKPTOLKEKNTMDLYVEKKKAQPLFFHNKEGSTSFTFRRDGMGTSSFESSRAYPOWF 127
Db	63 GGSQCLSGCTEGK-PILKIEPVNIMELYIGAKESISFTFRRDGMGTSSFESSRAYPOWF 121



GenCore version 4.5
 Copyright (c) 1993 - 2000 Compugen Ltd.

M protein - protein search, using sw model

run on: May 10, 2002, 09:09:50 ; Search time 12.56 seconds
 (without alignments)

maximum DB seq length: 0
 (without alignments)
 281.291 Million cell updates/sec

total number of hits satisfying chosen parameters: 212252

minimum DB seq length: 0
 (without alignments)

post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

result No.	Score	Query Length	DB ID	Description
1	452	55.3	164	Sequence 2, Appli
2	345.5	42.2	2	Sequence 2, Appli
3	345.5	42.2	169	Sequence 2, Appli
4	262	32.0	71	Sequence 4, Appli
5	20.5	155.4	0	Sequence 5, Appli
6	19.5	23.9	178	Sequence 21, Appli
7	19.5	23.9	178	Sequence 21, Appli
8	19.5	23.9	178	Sequence 21, Appli
9	18.7	22.9	185	Sequence 9, Appli
10	18.6	22.7	153	Sequence 18, Appli
11	18.6	22.7	153	Sequence 2, Appli
12	18.6	22.7	153	Sequence 2, Appli
13	18.6	22.7	388	Sequence 2, Appli
14	18.6	22.7	4	Sequence 14, Appli
15	18.3	22.4	178	Sequence 23, Appli
16	18.3	22.4	3	Sequence 10, Appli
17	18.2	22.4	178	Sequence 5, Appli
18	18.2	22.3	115	Sequence 9, Appli
19	18.2	22.3	115	Sequence 13, Appli
20	18.2	22.3	115	Sequence 11, Appli
21	18.2	22.3	136	Sequence 7, Appli
22	18.2	22.3	167	Sequence 2, Appli
23	18.2	22.3	178	Sequence 10, Appli
24	18.2	22.2	156	Sequence 10, Appli
25	18.2	22.2	2	Sequence 10, Appli
26	18.2	22.2	156	Sequence 10, Appli
27	18.2	22.2	159	Sequence 2, Appli

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
 US-08-939-300-2
 Sequence 2, Application US/08939300
 Patent No. 5945310
 GENERAL INFORMATION:
 APPLICANT: Young, Peter R.
 APPLICANT: Connor, Janice R.
 TITLE OF INVENTION: A No. 545310el Member of Family, ILI-1 Delta
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: RATNER & PRESTIA
 STREET: P.O. BOX 980
 CITY: VALLEY FORGE
 STATE: PA
 COUNTRY: USA
 ZIP: 19482

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/939,300
 FILING DATE: 29-SEP-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/046, 957
 FILING DATE: MAY 19, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: PRESTIA, PAUL F
 REGISTRATION NUMBER: 23, 031
 REFERENCE/DOCKET NUMBER: GH-70018
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEFAX: 610-407-0701
 TELEX: 846169
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 164 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ; US-08-939-300-2

Query Match Best Local Similarity 55.3%; Score 452; DB 2; Pred. No. 1.5e-433

ESULT 1
S-08-939-300-2
Sequence 2, Application US/08939300
patent No. 5945310

GENERAL INFORMATION:

APPLICANT: Young, Peter R.
APPLICANT: James, Ian E.
APPLICANT: Connor, Janice R.

TITLE OF INVENTION: A No. 5945310el Member of the IL-1 Delta

NUMBER OF INVENTION: Family, IL-1 Delta

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: RANTNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/939,300
FILING DATE: 29-SEP-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/046,957
FILING DATE: May 19, 1997

ATTORNEY/AGENT INFORMATION:

NAME: PRESTA, PAUL F

REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH 70018

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701

TELEX: 846169

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 164 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

S-08-939-300-2

ALIGNMENTS

28 182 22.2 159 2 US-08-444-598-2 Sequence
29 182 22.2 159 2 US-08-449-092-2 Sequence
31 182 22.2 159 2 US-08-449-814-2 Sequence
32 182 22.2 159 2 US-08-435-233-2 Sequence
33 182 22.2 159 2 US-08-471-227-3 Sequence
34 182 22.2 159 3 US-08-449-140-2 Sequence
35 182 22.2 159 4 US-08-417-455-14 Sequence
36 182 22.2 177 1 US-08-422-655-2 Sequence
37 182 22.2 177 2 US-08-849-185-2 Sequence
38 182 22.2 177 3 US-09-000-630-20 Sequence
39 182 22.2 177 3 US-08-842-730-20 Sequence
40 182 22.2 177 3 US-09-138-155-14 Sequence
41 182 22.2 177 4 US-09-417-455-30 Sequence
42 182 22.2 180 1 US-08-446-860-13 Sequence
43 182 22.2 180 2 US-08-910-733-13 Sequence
44 182 22.2 180 2 US-08-910-884-13 Sequence
45 178.5 21.8 177 3 US-09-000-630c-22 Sequence

Matches 88; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 MNPIOREAAPSKYATRDSRQWVWLGSNSLTAAPLSRSIKPVTLHLACRDTESDKEKGN 60
 Db 1 MNFQREAAPSKYATRDSRQWVWLGSNSLIAAPLSRSIKPVTLHLACRDTESDKEKGN 60
 Qy 61 MWVLGIGKDKCLCFAEIQGKPTLQIKEKNMD 93
 Db 61 MWVLGIGKDKCLCFAEIQGKPTLQIKEKNMD 93
 RESULT 2
 US-08-90-032-2
 Sequence 2; Application US/08790032
 Patent No. 5863769
 GENERAL INFORMATION:
 APPLICANT: Young, Peter
 TITLE OF INVENTION: Interleukin-1 Receptor Antagonist
 TITLE OF SEQUENCES: 2
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SmithKline Beecham Corporation
 STREET: 709 Swedeland Road
 CITY: King of Prussia
 STATE: PA
 ZIP: 19406-0939
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/790,032
 FILING DATE: 28-JAN-1997
 CLASSIFICATION: 536
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Schreck, Patricia A
 REGISTRATION NUMBER: 33,777
 REFERENCE/DOCKET NUMBER: ATG50051
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-270-5031
 TELEX:
 TELEFAX: 610-270-5090
 INFORMATION FOR SEQ ID NO: 2:
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 169 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-790-032-2
 Query Match 42.2%; Score 345.5; DB 2; Length 169;
 Best Local Similarity 45.0%; Pred. No. 1.8e-31;
 Matches 68; Conservative 29; Mismatches 53; Indels 1; Gaps 1;
 Qy 4 QREAAPSKYATRDSRQWVWLGSNSLIAAPLSRSIKPVTLHLACRDTESDKEKGN 63
 Db 17 QSMCKPITGTINDLNQWVTLQGQNIVAVERSDSVIFPVTVAVITCKYPEALEQGRGDPIY 76
 Qy 64 LGTKGKDCLCFAEIQGKPTLQIKEKNMDLYVERKAQPFLEFFHNGESTSVEQSVP 123
 Db 77 LGIQNPEMCLYCEKVGEOPTLQIKEQKIMDLYGOPEPVKFLFRAKTGRTSTLESVAFP 136
 Qy 124 GWFATTSITSGQPIFLKRGITNNFYLD 154
 Db 137 DWFIASSKRQ-QPIILTSELGKSYNTAFLN 166
 RESULT 4
 US-08-939-300-4
 Sequence 4; Application US/08939300
 Patent No. 5945310
 GENERAL INFORMATION:
 APPLICANT: Young, Peter R.
 APPLICANT: James, Ian E.
 APPLICANT: Connor, Janice R.
 TITLE OF INVENTION: A NO. 5945310el Member of the IL-1

RESULT 3
 US-09-069-19-2
 Sequence 2; Application US/09069619
 Patent No. 6054559
 GENERAL INFORMATION:
 APPLICANT: Young, Peter and Lisa Marshall
 TITLE OF INVENTION: Interleukin-1 Receptor Antagonist
 TITLE OF INVENTION: Beta (IL-1RA-)
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SmithKline Beecham Corporation
 STREET: 709 Swedeland Road
 CITY: King of Prussia
 STATE: PA
 ZIP: 19406-0939
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/069,619
 FILING DATE: Herewith
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 REGISTRATION NUMBER: 34,344
 REFERENCE/DOCKET NUMBER: ATG50051-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-270-5219
 TELEX:
 TELEFAX: 610-270-5090
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 169 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-069-619-2
 Query Match 42.2%; Score 345.5; DB 3; Length 169;
 Best Local Similarity 45.0%; Pred. No. 1.8e-31;
 Matches 68; Conservative 29; Mismatches 53; Indels 1; Gaps 1;
 Qy 4 QREAAPSKYATRDSRQWVWLGSNSLIAAPLSRSIKPVTLHLACRDTESDKEKGN 63
 Db 17 QSMCKPITGTINDLNQWVTLQGQNIVAVERSDSVIFPVTVAVITCKYPEALEQGRGDPIY 76
 Qy 64 LGTKGKDCLCFAEIQGKPTLQIKEKNMDLYVERKAQPFLEFFHNGESTSVEQSVP 123
 Db 77 LGIQNPEMCLYCEKVGEOPTLQIKEQKIMDLYGOPEPVKFLFRAKTGRTSTLESVAFP 136
 Qy 124 GWFATTSITSGQPIFLKRGITNNFYLD 154
 Db 137 DWFIASSKRQ-QPIILTSELGKSYNTAFLN 166
 RESULT 4
 US-08-939-300-4
 Sequence 4; Application US/08939300
 Patent No. 5945310
 GENERAL INFORMATION:
 APPLICANT: Young, Peter R.
 APPLICANT: James, Ian E.
 APPLICANT: Connor, Janice R.
 TITLE OF INVENTION: A NO. 5945310el Member of the IL-1

```

; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-417-455-5

RESULT          5
US-09-000-630C-21          24.5%; Score 200.5; DB 4; Length 155;
Best Local Similarity      35.1%; Pred. No. 3.8e-15; Gaps
Matches 54; Conservative   35.1%; Pred. No. 3.8e-15; Gaps
; Mismatches 24; Indels 15; Gaps
; 6;

QY          12 YAIRDSRQMWWLGSNLLAIPR-SRSIKVTLHILACR-DTERSDKEKGKGNMVLGK 67
Db          9 FRMKDSALKVLYLHNNOALLAGGIHAGKVKGEEISVWPNRWLDASLSP-----VIGVQ 62
QY          68 GKDLCIFCAEIQGKPTLQLKKEKNIMDLYVERKAQKFPLFHNGEGSTSFSVOSVSPWF 127
Db          63 GGSQLCLSCG-VGQEPIVTEPVNIMLYLAKESKSFYFRDMGLTSSFESAAYPGWFL 121
QY          128 ATSTSGOPITILTK--ERGITNN--TNFYLDSVE 157
Db          122 CTVPEADQVRLQPENGWGNAPITDFYFQQCD 155

```

Query Match

Sequence 21, Application US/09000630C

Patent No. 6018029

GENERAL INFORMATION:

APPLICANT: Fuller, Gerald M

APPLICANT: Fuente, Nelson L.

TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor

TITLE OF INVENTION: Antagonist

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Douglas C Murdock / Bradley, Arant, Rose & White

STREET: 2001 Park Place, Suite 1400

CITY: Birmingham

STATE: Alabama

COUNTRY: USA

ZIP: 35203-2736

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch,

COMPUTER: IBM compatible

OPERATING SYSTEM: Microsoft Windows

SOFTWARE: WordPerfect 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/000,630C

APPLICATION NUMBER: US/09/000,630C

FILED DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/862,730

APPLICATION NUMBER: 08/862,730

FILED DATE:

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

TYPE: amino acid

STRANDEDNESS: single

LENGTH: 178 amino acids

TOPOLOGY: linear

MOLECULE TYPE: mouse IL-1ra sequence

US-09-000-630C-21

Query Match 23.9%; Score 195.5; DB 3; Length 178;
 Best Local Similarity 33.6%; Pred. No. 1.7e-14; Matches 49; Conservative 23; Mismatches 49; Indels 25; Gaps 3;

QY 4 QREAAPKSYAIRDSRQMVWLSNSLIAAPL-SRSIK-----PVTIHLIACRDTERS 54 ; Patent No. 6294655
 Db 31 KRPCKMKAQFRIDTNQTFYLRLNQLIAGYLQGPNIKLEGKIDMVPIDLH----- 80 ; GENERAL INFORMATION:
 QY 55 DKEKGNAVYLGIGKGDCLFCATIQGKPTQPLQEKENIMDLYVEKKAKQPFLEFFHNKEGST 114 ; APPLICANT: Ford, John
 Db 81 -----SVFLGIHGKLQLSCAKSGDDIKLQLEEVNTIDSKNEEDKRFTRSEKGPT 134 ; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
 QY 115 SVFQSVPSPGWFIATSTSGQPIFLT 140 ; FILE REFERENCE: 28110/36528
 Db 135 TSFESACACPGWFCLTLEADRPVSLT 160 ; CURRENT APPLICATION NUMBER: US/09/417,455
 ; CURRENT FILING DATE: 1999-10-13
 ; PRIORITY NUMBER: US 09/348 942
 ; PRIORITY NUMBER: PCT/US99/04291
 ; PRIORITY NUMBER: US 09/287,210
 ; PRIORITY FILING DATE: 1999-04-05
 ; PRIORITY NUMBER: US 09/251,370
 ; PRIORITY FILING DATE: 1999-02-17
 ; PRIORITY APPLICATION NUMBER: US 09/229,591
 ; PRIORITY FILING DATE: 1999-01-13
 ; PRIORITY APPLICATION NUMBER: US 09/127,698
 ; PRIORITY FILING DATE: 1998-07-31
 ; PRIORITY APPLICATION NUMBER: US 09/099,818
 ; PRIORITY FILING DATE: 1998-06-19
 ; PRIORITY APPLICATION NUMBER: US 09/082,364
 ; PRIORITY FILING DATE: 1998-05-20
 ; PRIORITY APPLICATION NUMBER: US 09/079,909
 ; PRIORITY FILING DATE: 1998-05-15
 ; PRIORITY APPLICATION NUMBER: US 09/055,010
 ; PRIORITY FILING DATE: 1998-04-03
 ; NUMBER OF SEQ ID NOS: 30
 ; SEQ ID NO: 9
 ; LENGTH: 178
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-09-417-455-9

RESULT 7

US-08-862-730C-21

; Sequence 21, Application US/08862730C
 ; Patent No. 6063600
 ; GENERAL INFORMATION:
 ; APPLICANT: Fuller, Gerald M
 ; ATTORNEY: Fuentes, Nelson L
 ; TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Douglas C Murdock/ Bradley, Arant, Rose & White
 ; STREET: 2001 Park Place, Suite 1400
 ; CITY: Birmingham
 ; STATE: Alabama
 ; COUNTRY: USA
 ; ZIP: 35203-2736

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch,
 COMPUTER: IBM compatible
 OPERATING SYSTEM: Microsoft Windows
 SOFTWARE: WordPerfect 6.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/862,730C
 FILING DATE: 5/23/97
 INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 LENGTH: 178 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: mouse IL-1ra sequence
 ; US-08-862-730C-21

Query Match 23.9%; Score 195.5; DB 3; Length 178;
 Best Local Similarity 33.6%; Pred. No. 1.7e-14; Matches 49; Conservative 23; Mismatches 49; Indels 25; Gaps 3;

QY 4 QREAAPKSYAIRDSRQMVWLSNSLIAAPL-SRSIK-----PVTIHLIACRDTERS 54 ; Patent No. 6294655
 Db 31 KRPCKMKAQFRIDTNQTFYLRLNQLIAGYLQGPNIKLEGKIDMVPIDLH----- 80 ; GENERAL INFORMATION:
 QY 55 DKEKGNAVYLGIGKGDCLFCATIQGKPTQPLQEKENIMDLYVEKKAKQPFLEFFHNKEGST 114 ; APPLICANT: Pan, Yang
 Db 81 -----SVFLGIHGKLQLSCAKSGDDIKLQLEEVNTIDSKNEEDKRFTRSEKGPT 134 ; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
 QY 115 SVFQSVPSPGWFIATSTSGQPIFLT 140 ; FILE REFERENCE: 0910/052001
 Db 135 TSFESACACPGWFCLTLEADRPVSLT 160 ; CURRENT APPLICATION NUMBER: US/09/128,155
 ; CURRENT FILING DATE: 1998-08-03
 ; EARLIER APPLICATION NUMBER: US 60/091,650
 ; EARLIER FILING DATE: 1998-07-02
 ; EARLIER APPLICATION NUMBER: US 60/054,646
 ; EARLIER FILING DATE: 1997-08-04
 ; NUMBER OF SEQ ID NOS: 18
 ; SEQ ID NO: 18
 ; LENGTH: 185

RESULT 8

US-09-417-55-9

; Sequence 9, Application US/09417455

TYPE: PRT
ORGANISM: Artificial sequence

FEATURE:
NAME/KEY: synthetically generated
LOCATION: (1)..(185)

OTHER INFORMATION: predicts presence of alternatively spliced exons for a protein of
OTHER INFORMATION: interest in a stretch of genomic DNA
NAME/KEY: VARIANT
LOCATION: (1)..(185)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-128-155-18

Query Match 22.9%; Score 187; DB 3; Length 185;
Best Local Similarity 39.0%; Pred. No. 1.6e-13; Indels 10; Gaps 4;
Matches 39; Conservative 25; Mismatches 26; Indels 10; Gaps 4;

QY 57 EKGNMNVYLGIKGKDGLFCAEIQGK--PTLQKEKNIMDLVVEKKAKQPFLFFHNEGS 113
Db 81 EKGSPILLGSKGERCILYCKDQGSHPSLQLEK-LMKLAQKESARRPFFYRQVG 139

QY 114 TSFEGSVSYSPGWFIATSTTSQQPIFRKTKEQITNNNFYL 153
Db 140 WNMLESSAAHPGPOFCTSCNCNEPV----GIXNXVDFFL 173

RESULT 10
US-08-798-414-2
Sequence 2, Application US/08798414
Patient No. 6096728

GENERAL INFORMATION:
APPLICANT: COLLINS, David S.

APPLICANT: BEVILACQUA, Michael P.
TITLE OF INVENTION: COMPOSITION AND METHOD FOR TREATING
TITLE OF INVENTION: INFLAMMATORY DISEASES
NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: US
ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,414
FILING DATE: 07-FEB-1997
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,419
FILING DATE: 09-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,789
FILING DATE: 06-DEC-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US (Atty Dkt# A-365B-P)
FILING DATE: 23-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: ZINDRICK, Thomas D.
REGISTRATION NUMBER: 32,185
REFERENCE/DOCKET NUMBER: A-365C
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 153 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein

US-08-798-414-2

Query Match 22.7%; Score 186; DB 4; Length 153;
Best Local Similarity 29.4%; Pred. No. 1.6e-13; Indels 30; Gaps 5;
Matches 50; Conservative 22; Mismatches 68; Indels 30; Gaps 5;

QY 1 MNPOREAAPKSYAIR-DSRQMVWLSGNSTIAAPLRS-----SIKPYTLHLIACR 49
Db 1 MRPSGRKSSKMQAFRIVDQNQTKYFLRNNOVLYQGPNNVLEEKIDVYEPHAL--- 57

QY 50 DTEFSDEKGKMYVLGIKGKDGLFCAEIQGK--PTLQKEKNIMDLVVEKKAKQPFLFFH 109
Db 58 -----FLGHGGMCLSCVKSGDTRQLEAVNTDLSNRQDKRFAFIRS 104

QY 110 REGTSVFOSYSPGWFIATSTTSQQPIFRKTKEQITNNNFYL 157
Db 105 DSQPTTSFEAACPGMFLCTAMEADOPVSLSNMPDEGM-VTKFYQED 153

RESULT 11
US-09-131-247-2
Sequence 2, Application US/09131247
Patient No. 6294170

GENERAL INFORMATION:

APPLICANT: Boone, Thomas C.
APPLICANT: Hershenson, Susan

APPLICANT: Collins, David S.
APPLICANT: Bevilacqua, Michael P.

TITLE OF INVENTION: COMPOSITION AND METHOD FOR TREATING INFLAMMATORY
FILE REFERENCE: A-365F

CURRENT APPLICATION NUMBER: US/09/131,247

CURRENT FILING DATE: 1998-08-07

EARLIER APPLICATION NUMBER: 60/055,185

EARLIER FILING DATE: 1997-08-08

EARLIER APPLICATION NUMBER: PCT/US 97/02131

EARLIER FILING DATE: 1997-02-10

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 153

TYPE: PRT
ORGANISM: Human
US-09-131-247-2

Query Match 22.7%; Score 186; DB 4; Length 153;
Best Local Similarity 29.4%; Pred. No. 1.6e-13; Indels 30; Gaps 5;
Matches 50; Conservative 22; Mismatches 68; Indels 30; Gaps 5;

QY 1 MNPOREAAPKSYAIR-DSRQMVWLSGNSTIAAPLRS-----SIKPYTLHLIACR 49
Db 1 MRPSGRKSSKMQAFRIVDQNQTKYFLRNNOVLYQGPNNVLEEKIDVYEPHAL--- 57

QY 50 DTEFSDEKGKMYVLGIKGKDGLFCAEIQGK--PTLQKEKNIMDLVVEKKAKQPFLFFH 109
Db 58 -----FLGHGGMCLSCVKSGDTRQLEAVNTDLSNRQDKRFAFIRS 104

QY 110 REGTSVFOSYSPGWFIATSTTSQQPIFRKTKEQITNNNFYL 157
Db 105 DSQPTTSFEAACPGMFLCTAMEADOPVSLSNMPDEGM-VTKFYQED 153

RESULT 12
US-09-131-247-4
Sequence 4, Application US/09131247
Patient No. 6294170

GENERAL INFORMATION:
APPLICANT: Boone, Thomas C.
APPLICANT: Hershenson, Susan

APPLICANT: Collins, David S.

; TITLE OF INVENTION: COMPOSITION AND METHOD FOR TREATING INFLAMMATORY
; DISEASES
; FILE REFERENCE: A-365F
; CURRENT APPLICATION NUMBER: US/09/131,247
; EARLIER APPLICATION NUMBER: 60/055,185
; EARLIER FILING DATE: 1997-08-08
; EARLIER APPLICATION NUMBER: PCT/US 97/02131
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 4
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Human
; US-09-131-247-4

Query Match 22.7%; Score 186; DB 4; Length 153;
Best Local Similarity 29.4%; Pred. No. 1; 6.e-13; Matches 50; Conservative 22; Mismatches 68; Indels 30; Gaps 5;

QY 1 MNPQREAPPSKYSAIR-DSRQMVWLSGNSLIAPLSR-----SIKVPTLHLIACR 49
Db 1 MRPSGRKSSKMQAFRIWDVNOKTFYLRNNOVLYGKGDLCIFCAEIQKPTLQKEKNIMDLYVERKAQKPFLEFFHN 109
QY 50 DTEFSDKERGNMVLGIGKGDLCIFCAEIQKPTLQKEKNIMDLYVERKAQKPFLEFFHN 109
Db 58 -----FLGIHGGMCLSCVSKSGETRLQLEAVNITDSENRKQDKRAFIIRS 104

QY 110 KEGSTSYOSVSPGWFATSTSQPIFLIK--ERGTNTNTNFYLDSE 157
Db 105 DSGPTTSFESAACPGFWLCTAMEADQPSLTINMPDEGVN-VTKFYFOEDE 153

RESULT 13
US-09-131-247-16
SEQUENCE 16 Application US/09131247
PATENT NO. 629410
GENERAL INFORMATION:
APPLICANT: Boone, Thomas C.
APPLICANT: Hershenson, Susan
APPLICANT: Bevilacqua, Michael P.
APPLICANT: Collins, David S.
TITLE OF INVENTION: COMPOSITION AND METHOD FOR TREATING INFLAMMATORY
TITLE OF INVENTION: DISEASES
FILE REFERENCE: A-365F
CURRENT APPLICATION NUMBER: US/09/131,247
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 60/055,185
EARLIER FILING DATE: 1997-08-08
EARLIER APPLICATION NUMBER: US/09/131,247
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 60/055,185
EARLIER FILING DATE: 1997-08-08
NUMBER OF SEQ ID NOS: 16
SEQ ID NO: 16
LENGTH: 388
TYPE: PRT
ORGANISM: Human
US-09-131-247-14

Query Match 22.7%; Score 186; DB 4; Length 389;
Best Local Similarity 29.4%; Pred. No. 5; 9.e-13; Matches 50; Conservative 22; Mismatches 68; Indels 30; Gaps 5;

QY 1 MNPQREAPPSKYSAIR-DSRQMVWLSGNSLIAPLSR-----SIKVPTLHLIACR 49
Db 237 MRPSGRKSSKMQAFRIWDVNOKTFYLRNNOVLYGKGDLCIFCAEIQKPTLQKEKNIMDLYVERKAQKPFLEFFHN 109
QY 50 DTEFSDKERGNMVLGIGKGDLCIFCAEIQKPTLQKEKNIMDLYVERKAQKPFLEFFHN 109
Db 294 -----FLGIHGGMCLSCVSKSGETRLQLEAVNITDSENRKQDKRAFIIRS 340

QY 110 KEGSTSYOSVSPGWFATSTSQPIFLIK--ERGTNTNTNFYLDSE 157
Db 341 DSGPTTSFESAACPGFWLCTAMEADQPSLTINMPDEGVN-VTKFYFOEDE 389

RESULT 15
US-09-000-30C-23
SEQUENCE 23 Application US/09000630C
PATENT NO. 6018029
GENERAL INFORMATION:
APPLICANT: Fuller, Gerald M.
APPLICANT: Fuentes, Nelson L.
TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Douglas C Murdock/ Bradley, Arant, Rose & White
STREET: 2001 Park Place, Suite 1400
CITY: Birmingham
STATE: Alabama
COUNTRY: USA
ZIP: 35203-2736
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
COMPUTER: IBM compatible
OPERATING SYSTEM: Microsoft Windows
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:

Query Match 22.7%; Score 186; DB 4; Length 388;
Best Local Similarity 29.4%; Pred. No. 5; 9.e-13; Matches 50; Conservative 22; Mismatches 68; Indels 30; Gaps 5;

QY 1 MNPQREAPPSKYSAIR-DSRQMVWLSGNSLIAPLSR-----SIKVPTLHLIACR 49
Db 1 MRPSGRKSSKMQAFRIWDVNOKTFYLRNNOVLYGKGDLCIFCAEIQKPTLQKEKNIMDLYVERKAQKPFLEFFHN 109
QY 50 DTEFSDKERGNMVLGIGKGDLCIFCAEIQKPTLQKEKNIMDLYVERKAQKPFLEFFHN 109
Db 58 -----FLGIHGGMCLSCVSKSGETRLQLEAVNITDSENRKQDKRAFIIRS 104

APPLICATION NUMBER: US/09/000,630C
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/862,730
FILING DATE:
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: rat IL-1ra sequence
US-09-000-630C-23

Query Match 22.4%; Score 183.5; DB 3; Length 178;
Best Local Similarity 31.9%; Pred. No. 3.8e-13; Matches 45; Mismatches 26; Indels 15; Gaps 2;
Matches 45; Conservative 26; Mismatches 55; Indels 15; Gaps 2;
QY 4 QREAAPKSVAIRDSRQMVWVLGSNLIA---APLRSIKPVTLHLIACRDTESFSKEKG 59
Db 31 KRPCKMQAFRIWDTNQTKFYLRNQLIAGYLOGPNPKLEEKIDMVPIDFRN----- 81
QY 60 NMVYLGIKDKDLCIFCAEIQGKPKIQLKEENIMDIYVEKAQKPLFFHNGKESSSVFQS 119
Db 82 --VFLGKLGKLCISCVKSGDDTKLQLEEVNITDLINKNEEDKRFTFIRSETGPFTSFES 139
QY 120 VSYRGWFWIAMSTWSGQPPIRLT 140
Db 140 LACPGWFCLCTLEADHPVSLT 160

Search completed: May 10, 2002, 09:11:15
Job time: 85 sec

